

Remarks

No new matter has been added. The specification has been amended to direct the entry of this sequence listing after the claims of the above identified application, to provide the SEQ ID NOs next to the specific sequences, to correct paragraph formatting, and to correct obvious typographical errors. The tables on pages 103-116 have been reformatted so that the sequence identifiers could be added to the tables while maintaining the proper page margins.

In accordance with 37 C.F.R. § 1.821(g), this submission includes no new matter.

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the Sequence Listing and the computer readable copy of the Sequence Listing submitted herewith in the above application are the same.

It is respectfully believed that this application is now in condition for examination. Early notice to this effect is respectfully requested.

Respectfully submitted,

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Version with markings to show changes made

In the Specification:

A sequence listing was added.

Please replace the paragraph beginning on page 1, line 2 with the following paragraph:

The present application is a continuation in part of 08/347,610, filed December 1, 1994, which is a continuation in part of U.S. Patent Application Ser. No. 08/159,339, filed Nov. 29, 1993, now U.S. Patent 6,037,135, which is a continuation in part of U.S. Patent Application Ser. No. 08/103,396, filed Aug. 6, 1993 (now abandoned), which is a continuation in part of U.S. Patent Application Ser. No. 08/027,746, filed Mar. 5, 1993 (now abandoned), which is a continuation in part of U.S. Patent Application Ser. No. 07/926,666, filed Aug. 7, 1992 (now abandoned). The present application is also related to U.S. Patent Application Ser. No. 08/186,266, filed January 25, 1994, now U.S. Patent 5,662,907, which is a continuation in part of U.S. Patent Application Ser. No. 08/159,339 as described above. All of the above applications and patents are hereby incorporated by reference as if fully set forth.

The paragraph beginning on page 55, line 12 was replaced with the following paragraph:

As a radiolabeled probe, the peptide 941.12 (KVFPYALINK) (SEQ ID NO:52), containing an A3.2 motif, was used. This peptide contains the anchor residues V₂ and K₁₀,

associated with A3.2-specific binders, described above. A Y residue was inserted at position 5 to allow for radioiodination ~~radioiodination~~. Peptides were labeled by the use of the Chloramine T method, Buus et al., Science 235:1352 (1987), which is incorporated herein by reference.

The paragraph beginning on page 57, line 11 was replaced with the following paragraph:

The cell line BVR was used as a source of HLA. The dependency of the binding on MHC concentration in presence or absence of β_2M are shown in Fig. 6, while Fig. 7 depicts the dose dependency of the inhibition by excess unlabeled ligand. Finally, Fig. 8 shows a Scatchard analysis experiment. Values of apparent K_D of ~ 6 nM and of 10% active receptor were obtained, and were remarkable for their similarity to the values obtained for A2.1 and A3.2. The sequence of the peptide used as a radiolabeled probe (940-06) is AVDLYHFLK (SEQ ID NO:53).

The paragraph beginning on page 57, line 22 was replaced with the following paragraph:

In this case, the EBV cell line Steinlin was used as a source of purified HLA. The same protocol previously applied to purification of other HLA alleles (i.e., depletion of B, C molecules by a B1.23.2 mAb column, followed by purification of A molecules by means of a W632 mAb column) was utilized. On the basis of the pool sequencing data, consensus peptides were synthesized, directly radiolabeled, and tested for HLA binding using the standard protocol (1 mM β_2M , 2 days RT incubation in presence of protease inhibitors). A

graph illustrating the relationship between % binding and μ M input HLA A1 is shown in Fig. 9. From the data, it was concluded that in analogy with what was observed for HLA A2, 3, and 11, as little as 30 nM are sufficient to obtain \sim 10% binding. The sequence of the peptide used as a radiolabeled probe (944.02) is YLEPAIAKY (SEQ ID NO:54). In the next set of experiments, the specificity of the assay established was verified by its ~~inhabitability~~ inhibitability by excess unlabeled peptide. The IC50% was measured (Fig. 10) as \sim 20 nM. Further Scatchard analysis (Fig. 11) verified that the apparent K_D of the interaction corresponded to 21 nM, with a % of active receptor corresponding to 5.1%.

The paragraph beginning on page 58, line 6 was replaced with the following paragraph:

HLA A24 molecules were purified from the KT3 EBV cell line. In this case, two consensus peptides whose sequences were based on the pool sequencing data have been synthesized. Their sequences are: 979-01, AYIDNVYKF (SEQ ID NO:55) and 979.02, AYIDNYNKF (SEQ ID NO:56). The results of experiments in which the % bound of these two peptides as a function of input MHC was measured are shown in Fig. 12. In both cases, 10-15% binding was obtained with as little as 20-50 nM MHC. Cold inhibition experiments (Fig. 13), limiting MHC concentrations, revealed that the binding was readily inhibitable by excess unlabeled peptide, with an apparent K_D of 30 and 60 nM, respectively. Further Scatchard experiments verified values of 136 nM and 28 nM, respectively. The apparent % of available receptor (active MHC) were 8.3% and 7.4%, respectively (Fig. 9a and b). On the basis of these data, peptide 979.02 was arbitrarily selected as standard label indicator for A24 assays. Furthermore, on the basis of the data herein described, we also conclude

that the goal of establishing an A24-specific binding assay has been accomplished. In conclusion, specific assays for the five major HLA alleles have been described.

The paragraph beginning on page 59, line 5 was replaced with the following paragraph:

For example, in the case of A3.2, a motif has been defined with a hydrophobic residue in position 2 and a positive charge (K) in position 9. Thus, to verify that the presence of these two anchor residues would allow, in the context of a poly A backbone, for A3.2 binding, the poly A analog with the sequence AMAAAAAAK (SEQ ID NO:61) was synthesized (Table 13).

The paragraph beginning of page 65, line 30 was replaced with the following paragraph:

Table 20(b) describes the peptides that bound to HLA-A3.2 molecules. Seven peptides were identified as high affinity binders, 6 as intermediate affinity binders and 13 as low affinity binders. Table 20(c) describes the peptides that bound to HLA-A11.2 molecules. Six high affinity peptides were identified, 4 intermediate affinity binders and 10 low affinity binders. Two high affinity binding peptides (E6-59 IVYRDGNPY (SEQ ID NO:142) and E6-80 ISEYRHYAY (SEQ ID NO:132)) and two weak affinity binding peptides with a Y at the 9th position (E6-42 QQLLRREVY (SEQ ID NO:155), E6-69 VADKALKFY (SEQ ID NO:133)) were identified for HLA-A11.2. Considering the high binding strength of the first two peptides and the similarity between the HLA-A11.2 motif and the HLA-A3.2 motif in which Y's are preferred at the 9th aa position, tyrosines should

be included at the 9th position in the HLA-A11.2 motif. Comparing Tables 21(b) and (c) it is clear that there is a large overlap of peptides that bound to both A3.2 and A11.2 molecules. Eighteen out of 28 E6 and E7 peptides binding to these two HLA molecules overlapped and only 8 peptides were unique for HLA-A3.2 and 2 peptides unique for HLA-A11.2.

The paragraph beginning on page 66, line 11 was replaced with the following paragraph:

Finally, Table 20(d) describes the peptides that bound to HLA-A24 molecules. Here 2 peptides were identified as high affinity binding peptides, 5 as intermediate affinity binding peptides and 5 as low binding peptides. One high affinity peptide (E6-72 KALKFYSKI) (SEQ ID NO:168) and one intermediate affinity peptide (E7-49 RAHYNIVTF) (SEQ ID NO:170) were identified, indicating that an A at the second position should be allowed in the HLA-A24 motif. All these inclusions are indicated in Table 20-e. In analyzing these tables it can be concluded that between 2 and 7 high affinity binding peptides were identified for all of the tested HLA-A molecules. Occasionally some peptides were binding to more alleles. Three peptides (E6-7, E6-37 and E6-79), bound to HLA-A2.1, A3.2 and A11.2. One peptide (E6-38) bound to HLA-A3.2, A11.2 and A24 and two peptides (E6-69 and E6-80) bound to HLA-A1, A3.2 and A11.2. But these crossreactive peptides bound only weakly to one or more of the different HLA molecules. In general, however, it can be concluded that, except for HLA-A3.2 and HLA-A11.2 molecules, almost all HLA molecules bind unique peptides.

Please replace the paragraph beginning on page 87, line 34 with the following paragraph:

All of the references cited herein, including patents, patent applications, and publications, are hereby incorporated in their entireties by reference.

Pending pages 50-54 were replaced with the attached substitute pages 50-54.

Pending pages 88-97 were replaced with the attached substitute pages 88-97.

Pending pages 103-117 were replaced with the attached substitute pages 103-117.

Version with markings to show changes made

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For HLA-A11 (A*1101):

5
1 XTXXXXXXXXK
2 XTXXXXXXXXK
3 XVXXXXXXXXK
4 XVXXXXXXXXK

For HLA-A24.1 (A*2401):

10
1 XYXXXXXXXXF
2 XYXXXXXXXXF
3 XYXXXXXXXXL
4 XYXXXXXXXXL

Peptides with MHC Class I Binding Motifs

Table 9

deleted

added

Peptides with MHC Class I Binding Motifs Table 9

AA Position	Sequence (SEQ ID NO)	Antigen	HLA molecule
5	30 IHDIILECVY (1)	HPV16.E6	A1
	69 VCDKCLKFY (2)	HPV16.E6	A1
	77 YSKISEYRHY (3)	HPV16.E6	A1
	80 ISEYRHYCY (4)	HPV16.E6	A1
	92 GTTLEQQYNK (5)	HPV16.E6	A11
10	93 TTLEQQYNK (6)	HPV16.E6	A11
	106 LLIRCINCQK (7)	HPV16.E6	A3
15	2 HGDTPTLHEY (8)	HPV16.E7	A1
	16 QPETTDLYCY (9)	HPV16.E7	A1
	44 QAEPDRAHY (10)	HPV16.E7	A1
	89 IVCPICSQK (11)	HPV16.E7	A3, A11
20	3 RFEDPTRRPY (12)	HPV18.E6	A1
	4 FEDPTRRPY (13)	HPV18.E6	A1
	25 LQDIEITCVY (14)	HPV18.E6	A1
	41 LTEVFEFQFK (15)	HPV18.E6	A11
	72 YSRIRELRHY (16)	HPV18.E6	A1
	84 SVYGDITLEK (17)	HPV18.E6	A3, A11
25	101 LLIRCLRCQK (18)	HPV18.E6	A3
	59 HTMLCMCK (19)	HPV18.E7	A11

added

Human Papilloma Virus 16 and 18 (E6 and E7 Proteins)

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Peptides with MHC Class I Binding Motifs Table 10

added

AA Position	Sequence (SEQ ID NO)	Antigen	HLA molecule
5	2 SLEQRS LHCK (20)	MAGE 1	A3
	96 SLFRAVITK (21)	MAGE 1	A3
	96 SLFRAVITKK (22)	MAGE 1	A3
	108 DLVGFLLLK (23)	MAGE 1	A3
	128 MLESVIK NYK (24)	MAGE 1	A3
10	128 MLESVIK NY (25)	MAGE 1	A1
	152 QLVFGIDVK (26)	MAGE 1	A3
	161 EADPTGHSY (27)	MAGE 1	A1
	182 LLGDNQIMPK (28)	MAGE 1	A3
	215 WEELSVMEVY (29)	MAGE 1	A1
15	223 VYDGREHSAY (30)	MAGE 1	A1
	238 LLTQDLVQEK (31)	MAGE 1	A3
	239 LTQDLVQEK (32)	MAGE 1	A11
	239 LTQDLVQEKY (33)	MAGE 1	A1
20	240 TQDLVQEKY (34)	MAGE 1	A1

Melanoma Antigen MAGE 1

Version with markings to show changes made

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Peptides with MHC Class I Binding Motifs Table 11

added

AA Position	Sequence (SEQ ID NO:)	Antigen	HLA molecule
5	21 IVGGWECEK (35)	PSA	A3, A11
	57 LTAAHCIRNK (36)	PSA	A11
	88 VSHSFPHPLY (37)	PSA	A1
	95 PLYDMSLLK (38)	PSA	A3
	178 DVCAQVHPQK (39)	PSA	A3, A11
10	182 QVHPQKVTK (40)	PSA	A3, A11
	236 PSLYTKVVHY (41)	PSA	A1
	239 YTKVVHYRK (42)	PSA	A11
	241 KVVHYRKWIK (43)	PSA	A3, A11
	242 VVHYRKWIK (44)	PSA	A3, A11
15			

Prostate Specific Antigen (PSA)

Version with markings to show changes made

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Peptides with MHC Class I Binding Motifs Table 12

added

AA Position	Sequence (SEQ ID NO:)	Antigen	HLA molecule
5	2 STNPKPQRK (45)	HCV	A11
	14 NTNRRPQDVK (46)	HCV	A11
	43 RLGVRATRK (47)	HCV	A3
	302 VQDCNCSIY (48)	HCV	A1
	556 WMNSTGFTK (49)	HCV	A3
10	605 LTPRCMVDY (50)	HCV	A1
	626 FTIFKIRMY (51)	HCV	A1

Hepatitis C Virus (Consensus Sequence)

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Version with markings to show changes made

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TABLE 13

VALIDATION OF CYTEL'S HLA MOTIFS

5	Binding Capacity (IC ₅₀ nM)						
	Sequence	Motif	A1	A2.1	A3.2	A11	A24
	AADKAAAAAY	A1	50	--*	--	--	--
	ATAKAAAAAY	A1	15	--	329	77	--
	ATDKAAAAAY	A1	2.8	--	9250	840	ND
10	ALAKAAAAV	A2.1	--	125	--	--	--
	AMAAAAAAK	A3.2	--	--	48	8.4	--
	ATAAAAAAK	A11	--	--	59	40	--
	AYAKAAAAF	A24	--	--	--	--	115

15 *A dash indicates an IC₅₀ greater than 20,000 nM.

added

SEQ ID NO:
57
58
59
60
61
62
63

TABLE 14

20 *added* VALIDATION OF CYTEL'S HLA MOTIFS

20	Binding Capacity (IC ₅₀ nM)					
	SEQUENCE (SEQ ID NO)	MOTIF	A1	A2.1	A3.2	A11
	AADKAAAAAY (64)	A1	45	--*	--	--
25	ATAKAAAAAY (65)	A1	58	--	1100	1030
	ATDKAAAAAY (66)	A1	4.0	--	10000	4533
	ALAKAAAAV (67)	A2.1	ND	1400	--	--
	AMAAAAAAK (68)	A3.2	ND	--	85	24.0
	ATAAAAAAK (69)	A11	--	--	216	88

30 *A dash indicates an IC₅₀ greater than 20,000 nM.

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TABLE 15

HLA-A3.2

added

	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 952.25	SUBSTITUTION	SER ID No:
5	952.25	ALAAAAAAK	1	-	70
	952.26	AMAAAAAAK	1.2	position 2	61
	952.23	AVAAAAAAK	0.95		71
	981.04	ASAAAAAAK	0.89		72
10	952.24	AIAAAAAAK	0.57		73
	952.27	AAAAAAAK	0.57		74
	981.06	ATAAAAAK	0.49		62
	981.08	AFAAAAAAK	0.13		75
	981.09	AGAAAAAAK	0.077		76
15	981.13	ACAAAAAAK	0.031		77
	981.12	ADAAAAAAK	0.014		78
	981.11	ANAAAAAAK	0.0010		79
	981.05	AKAAAAAAK	<0.0016		80
	981.07	AYAAAAAAK	<0.0005		81
20	981.10	APAAAAAAK	<0.0006		82
	952.35	ALAAAAAAR	0.46	position 9	83
	981.36	ALAAAAAAY	0.15		84
	981.33	ALAAAAAAA	0.0034		85
	981.35	ALAAAAAAQ	<0.0006		86
25	981.37	ALAAAAAAS	<0.0005		87
	981.38	ALAAAAAAT	<0.0005		88
	981.34	ALAAAAAAN	<0.0005		89
	981.39	ALAAAAAAE	<0.0003		90

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TABLE 16

HLA-A11

added

	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 952.25	SUBSTITUTION	SEQ ID NO.
5	952.25	ALAAAAAAK	1		70
	952.26	AMAAAAAAK	2.5	position 2	61
	952.27	AAAAAAAK	1.1		74
	952.24	AIAAAAAAK	0.72		73
10	981.06	ATAAAAAAK	0.55		62
	981.04	ASAAAAAAK	0.46		72
	981.09	AGAAAAAAK	0.38		76
	952.23	AVAAAAAAK	0.23		71
	981.11	ANAAAAAAK	0.23		79
15	981.13	ACAAAAAAK	0.019		77
	981.08	AFAAAAAAK	0.020		75
	981.12	ADAAAAAAK	0.012		78
	981.05	AKAAAAAAK	0.0065		80
	981.07	AYAAAAAAK	<0.0065		81
20	981.10	APAAAAAAK	<0.0051		82
	952.35	ALAAAAAAR	0.015	position 9	83
	981.33	ALAAAAAAA	<0.0059		85
	981.34	ALAAAAAAN	<0.0071		89
	981.35	ALAAAAAAQ	<0.0051		86
25	981.36	ALAAAAAAY	<0.0071		84
	981.37	ALAAAAAAS	<0.0051		87
	981.38	ALAAAAAAT	<0.0051		88
30	981.39	ALAAAAAAE	<0.0071		90

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TABLE 17

HLA-A24

added

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 983.01	SUBSTITUTION	SEQ ID NO:
	983.01	AYAKAAAF	1	-	63
	983.08	AFAKAAAF	0.24	position 2	91
	983.09	APAKAAAF	0.0058		92
	983.10	AAAKAAAF	0.0023		93
10	983.11	AKAKAAAF	<0.0012		94
	983.05	AYAKAAAI	0.20	position 9	95
	983.04	AYAKAAAL	0.11		96
	983.06	AYAKAAAV	0.0023		97
	983.02	AYAKAAAA	<0.0012		98
15	983.03	AYAKAAAY	<0.0012		99
	983.07	AYAKAAAK	<0.0012		100

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TABLE 18

HLA-A1

added

	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 982.07	SUBSTITUTION	SEQ ID NO:
5	982.011	ATDKAAAAAY	Motif	-	59
	982.07	ATAKAAAAAY	1	-	58
	982.09	ASAKAAAAAY	0.17	position 2	101
	982.13	AMAKAAAAAY	0.095	no D in pos 3	102
10	982.08	AAAKAAAAAY	0.0064		103
	954.09	ALAKAAAAAY	0.0045		104
	954.11	AIKAAAAAY	0.0045		105
	954.13	AVAKAAAAAY	0.0020		106
	982.10	AKAKAAAAAY	0.0011		107
15	982.11	ANAKAAAAAY	<0.0001		108
	982.12	ADAKAAAAAY	<0.0001		109
	982.14	AGAKAAAAAY	<0.0001		110
	982.15	APAKAAAAAY	<0.0001		111
	982.16	AYAKAAAAAY	<0.0001		99
20	982.17	AHAKAAAAAY	<0.0001		112
	982.24	ATAKAAAAA	0.0040	position 9	113
	982.23	ATAKAAAAF	0.0019	no D in pos 3	114
	982.28	ATAKAAAAH	0.0010		115
	982.32	ATAKAAAAV	0.0005		116
25	982.25	ATAKAAAAN	<0.0001		117
	982.26	ATAKAAAAD	<0.0001		118
	982.27	ATAKAAAAW	<0.0001		119
	982.30	ATAKAAAAK	<0.0001		120
	982.31	ATAKAAAAI	<0.0001		121
30	982.29	ATAKAAAAP	<0.0001		122

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TABLE 19

HLA-A1

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 982.07	SUBSTITUTION	SEQ ID
					NO:
	982.01	ATDKAAAAAY	Motif	-	59
	982.07	ATAKAAAAAY	1	-	58
	982.01	AADKAAAAAY	0.14	position 3	57
	954.03	AAEKAAAAAY	0.038	no T in pos 2	123
10	982.02	AAAKAAAAAY	0.0055		103
	982.06	AASKAAAAAY	0.0024		124
	982.04	AANKAAAAAY	0.0011		125
	982.03	AAQKAAAAAY	0.0008		126
	982.05	AAKKAAAAAY	<0.0001		127
15	982.20	AADKAAAAA	0.0016	position 9	128
	982.21	AADKAAAAW	0.0005	no T in pos 2	129
	982.19	AADKAAAAF	<0.0001		130
	982.22	AADKAAAAK	<0.0001		131

added

Version with markings to show changes made

TABLE 20(A)

HPV16 E6 AND E7 PEPTIDES BINDING TO HLA-A1

5	Origin	First aa Position	Sequence	(Seq ID No:)	Binding Ratio to Standard:	Motif Prediction
	E6	80	ISEYRHYAY	(132)	3.500	+
	E6	69	VADKALKFY	(133)	0.240	+
	E7	44	QAEPRAHY	(134)	0.029	+
10	E7	37	EIDGPAGQA	(135)	0.025	-
	E7	19	TTDLYAYEQ	(136)	0.023	+
	E6	144	MSAARSSRT	(137)	0.019	+/-
	E7	73	HVDIRTLED	(138)	0.014	-
	E6	139	WTGRAMSAA	(139)	0.010	-
15	E6	61	YRDGNPYAV	(140)	0.008	-

* Bold A's indicate residues in which cysteine was replaced by alanine.

* The average IC₅₀ value \pm SE of the standard in the course of the experiments considered in this table was 81 \pm 30 nM. Listed in the table are peptides yielding ratio values of ≥ 0.001 . All other peptides yielded ratio values of ≤ 0.001 .

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TABLE 20(B)
HPV16 E6 and E7 Peptides Binding to HLA-A3.2

	Origin	First aa Position	Sequence	Seq. No. (No.)	Binding Ratio to Standard?	Motif Prediction
5	E6	107	LIRAINAQK	(141)	3.7000	+
	E6	59	IVYRDGNPY	(142)	3.0000	+
	E7	89	IVAPIASQK	(143)	2.2000	+
10	E6	33	IILEAVYAK	(144)	1.5000	+
	E6	125	HLDKKQRFH	(145)	0.4400	+
	E6	143	AMSAARSSR	(146)	0.1800	+
	E6	7	AMFQDPQER	(147)	0.1000	+
	E6	93	TTLEQQYNK	(148)	0.0780	+
15	E6	37	AVYAKQQLL	(149)	0.0320	-
	E7	51	HYNIVTFAA	(150)	0.0210	-
	E6	145	SAARSSRTR	(151)	0.0200	+
	E6	75	KFYISKISEY	(152)	0.0100	+
	E6	89	SLYGTTLQ	(153)	0.0080	-
20	E7	52	YNIVTFAAK	(154)	0.0067	-
	E6	80	ISEYRHYAY	(155)	0.0064	+
	E6	42	QQLLRREYV	(156)	0.0058	-
	E6	68	AVADKALKF	(157)	0.0056	+
	E6	97	QQYNKPLAD	(158)	0.0045	-
25	E6	79	KISEYRHYA	(159)	0.0044	-
	E6	84	RHYAYSLYG	(160)	0.0036	-
	E6	69	VADKALKFY	(161)	0.0025	+
	E6	146	AARSSRTRR	(162)	0.0020	+
	E7	58	AAKADSTLR	(163)	0.0016	+
30	E6	38	VYAKQQLLR	(164)	0.0012	-
	E6	67	YAVADKALK	(165)	0.0012	+
	E7	60	KADSTLRLA	(166)	0.0012	-

* Bold A's indicate residues in which cysteine was replaced by alanine.
 + The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 30±3 nM. Listed in the table are peptides yielding ratio value of ≥0.001. All other peptides yielded ratio values of <0.001.

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Table 20(C)

HPV16 E6 and E7 Peptides Binding to HLA-A11.2

	Origin	First aa Position	Sequence	Seq ID No.	Binding Ratio to Standard	Motif Prediction
5	E6	33	IILEAVYAK	(144)	6.7000	+
	E6	93	TTLEQQYNK	(148)	1.8000	+
	E7	89	IVAPIASQK	(143)	1.3000	+
10	E6	7	AMFQDPQER	(147)	0.8400	+/-
	E6	59	IVYRDGNPY	(142)	0.4700	- (+) ^S
	E6	80	ISEYRHYAY	(132)	0.4300	- (+) ^S
	E6	37	AVYAKQQLL	(149)	0.0450	-
	E6	145	SAARSSRTR	(151)	0.0330	+/-
15	E6	107	LIRAINAQK	(141)	0.0120	+
	E7	58	AAKADSTLR	(161)	0.0110	+/-
	E6	42	QQLLRREVV	(155)	0.0084	+/- (+) ^S
	E6	143	AMSAARSSR	(146)	0.0084	-
	E6	79	KISEYRHYA	(158)	0.0076	-
20	E6	67	YAVADKALK	(163)	0.0074	+
	E7	52	YNIIVTFAAK	(154)	0.0060	+
	E6	68	AVADKALKF	(156)	0.0037	-
	E6	69	VADKALKFY	(133)	0.0030	- (+) ^S
	E6	38	VYAKQQLLR	(162)	0.0022	+/-
25	E6	140	TGRAMSAAR	(165)	0.0012	+/-
	E7	90	VAPIASQKP	(166)	0.0012	-
	E7	51	HYNIIVTFAA	(150)	0.0010	-

* Bold A's indicate residues in which cysteine was replaced by alanine.

† The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 10±3 nM. Listed in the table are peptides yielding ratio value of ≥0.001. All other peptides yielded ratio values of ≤0.001.

§ Brackets indicate score according to adjusted motif.

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Table 20(D)

HPV16 E6 and E7 Peptides Binding to HLA-A24

5	Origin	First aa Position	Sequence	Seq ID (NO)	Binding Ratio to Standard	Motif Prediction
	E6	87	AYS LY GTTL	(167)	0.1200	+
	E6	72	KALKFY SK I	(168)	0.1100	- (+) ⁵
	E6	131	RFHNIRGRW	(169)	0.1000	+
10	E7	49	RAHYNIVTF	(170)	0.0670	- (+) ⁵
	E6	49	VYDFAFRDL	(171)	0.0610	+
	E6	82	EYRHYAYSL	(172)	0.0460	+
	E6	26	LQTTIHDII	(173)	0.0200	-
	E6	66	PYAVADKAL	(174)	0.0055	-
15	E6	1	MHQKRTAMP	(175)	0.0049	-
	E6	85	HYAYS LY GT	(176)	0.0037	-
	E6	44	LLRRE VY DF	(177)	0.0023	+
	E6	38	VYAKQQLLR	(162)	0.0011	-

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- ^{*} Bold A's indicate residues in which cysteine was replaced by alanine.
[†] The average IC₅₀ value \pm SE of the standard in the course of the experiments considered in this table was 22 \pm 6 nM. Listed in the table are peptides yielding ratio value of \geq 0.001. All other peptides yielded ratio values of \leq 0.001.
⁵ Brackets indicate score according to adjusted motif.
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Table 23(a)

added

Seq ID	Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
181	1.0300	HLDMLRHLY	9	c-ERB2			42	1	9.1	0.037	0.0002	
178	1.0346	LLDIDETEY	9	c-ERB2			869	1	7.6	0.0003	0	
179	1.0305	GTQLFEDNY	9	c-ERB2			104	1	0.18	0	0.028	
180	1.0355	LTCSPQPEY	9	c-ERB2			1131	1	0.13	0	0.0061	
181	1.0317	ETLEETICY	9	c-ERB2			401	1	0.043	<0.0002	<0.0002	
182	1.0749	FTHQSDVWSY	10	c-ERB2			899	1	2.7	0.0003	0.0005	
183	1.0747	RLLDIDETEY	10	c-ERB2			868	1	1.3	0.0017	0	
184	1.0715	TLEETGYLY	10	c-ERB2			402	1	1.1	0	0	
185	1.0737	YVMAGVCSPI	10	c-ERB2			772	1	1.1	0.010	0.012	0
186	1.0764	CTPTAENPEY	10	c-ERB2			1239	1	0.063	<0.0002	0.0022	
187	1.0705	LIQNPQLCY	10	c-ERB2			154	1	0.030	0.0012	<0.0002	
188	1.0693	VVQGNLELY	10	c-ERB2			55	1	0.018	0.0024	0.011	
189	1.0756	MGLVDAAEY	10	c-ERB2			1014	1	0.012	<0.0002	<0.0002	
190	1.1028	KIRKYTMKR	9	c-ERB2			681	3,11		0.76	0.0018	
191	1.1027	VVRGILKR	9	c-ERB2			669	3,11		0.11	0.72	
192	1.0944	LKSPNHYK	9	c-ERB2			852	3,11		0.48	0.070	
193	1.0835	VLRNTSPK	9	c-ERB2			754	3,11		0.40	0.013	
194	1.0829	ILIKRRQOK	9	c-ERB2			673	3,11		0.38	0.0097	
195	1.0911	ILWKDIFHK	9	c-ERB2			167	3,11		0.28	0.31	
196	1.1033	KITDFGLAR	9	c-ERB2			860	3,11		0.17	0.24	
197	1.0869	GVVRGILK	9	c-ERB2			668	3,11		0.0047	0.089	
198	1.0299	QVCTGTDMAK	9	c-ERB2			24	3,11		0.0007	0.052	
199	1.1031	LLDHVRENK	9	c-ERB2			806	3,11		0.037	<0.0006	
200	1.1026	CVNCSQFLR	9	c-ERB2			528	3,11		0.0015	0.031	
201	1.1023	TVGAGGQAR	9	c-ERB2			218	3,11		0.0004	0.023	
202	1.0831	ILKETELRK	9	c-ERB2			714	3,11		0.019	0.0023	
203	1.1024	VTAEDGTQR	9	c-ERB2			322	3,11		<0.0002	0.014	
204	1.0826	DLSYMPTWK	9	c-ERB2			607	3,11		0.0005	0.010	
205	1.0707	TILWKDIFHK	10	c-ERB2			166	3,11		0.043	3.6	
206	1.0712	GTQRCCKSK	10	c-ERB2			327	3,11		0.021	0.61	
207	1.0736	KVLRNTSPK	10	c-ERB2			753	3,11		0.38	0.22	
208	1.0702	QLRSLTEILK	10	c-ERB2			141	3,11		0.20	0.013	
209	1.1142	RLVHRDLAAR	10	c-ERB2			840	3,11		0.18	0	
210	1.0741	LLNWCNQIAK	10	c-ERB2			822	3,11		0.14	0.14	
211	1.0752	TIDVYMIMVK	10	c-ERB2			948	3,11		0.013	0.12	

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Table 23(a)
continued
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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0731	RILKETELRK	10	c-ERB2			713	3,11		0.057	0.11	
1.0745	VLVKSPNHVK	10	c-ERB2			851	3,11		0.082	0.0072	
1.1131	SVFQNLQVIR	10	c-ERB2			423	3,11		0.017	0.075	
1.1133	HTVPWDQLFR	10	c-ERB2			478	3,11		0.0035	0.072	
1.1127	ILKGGVLIQR	10	c-ERB2			148	3,11		0.040	0.0005	
1.1143	LVSEFSRMAR	10	c-ERB2			972	3,11		0.0072	0.033	
1.1136	GVVFGILIKR	10	c-ERB2			668	3,11		0.018	0.033	
1.0726	CVARCTPSGVK	10	c-ERB2			596	3,11		0.022	0.0042	
1.1137	VVFGILIKRR	10	c-ERB2			669	3,11		0.0030	0.016	
1.0728	GILKRRROOK	10	c-ERB2			672	3,11		0.015	0.0014	
1.1129	RTVCAGCCAR	10	c-ERB2			217	3,11		0.0068	0.013	
1.1134	GLACHQLCAR	10	c-ERB2			508	3,11		0.011	0	
1.1139	KIPVAIKVLR	10	c-ERB2			747	3,11		0.0009	0.0099	

Table 23(b)

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0291	VGEADYFEY	9	EBNA1			409	1	0.016			
1.0295	PLRESIVCY	9	EBNA1			553	1	0.010			
1.0681	PVGEADYFEY	10	EBNA1			408	1	0.015			
1.0683	GTWVAGVFVY	10	EBNA1			501	1	0.014			
1.0293	GVFVYGGSK	9	EBNA1			506	3,11		0.30	0.61	
1.1016	KTSLYNLRR	9	EBNA1			514	3,11		0.31	0.12	
1.0297	AIKDLVMTK	9	EBNA1			578	3,11		0.048	0.034	
1.0687	QTHFAEVLK	10	EBNA1			567	3,11		0.010	0.21	
1.1124	GTALAIPOCR	10	EBNA1			523	3,11		0.0028	0.056	

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Table 23(c)

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
5.0005	CTELKLSDY	9	FLU	A	NP	44	1	3.6			
5.0006	STLELRSY	9	FLU	A	NP	377	1	0.020			
5.0044	ILRGSAVHK	9	FLU	A	NP	265	3		1.5	0.0037	
5.0051	RMCNILGK	9	FLU	A	NP	221	3		0.27	0.062	
5.0046	LMQGSTLPR	9	FLU	A	NP	166	3		0.031	0.10	
5.0048	MIDGIGRFY	9	FLU	A	NP	32	3		0.059	0.0010	
5.0049	MVLSAFDER	9	FLU	A	NP	66	3		0.0016	0.041	
5.0054	YIQMCTELK	9	FLU	A	NP	40	3		0.0031	0.030	
5.0042	GINDRNPWR	9	FLU	A	NP	200	3		0.0028	0.024	
5.0104	SLMQGSTLPR	10	FLU	A	NP	165	3		0.12	0.84	
5.0095	KMIDGIGRFY	10	FLU	A	NP	31	3		0.50	0.0079	
5.0096	LILRGSAVHK	10	FLU	A	NP	264	3		0.36	0.037	
5.0102	PSGAAGAAVK	10	FLU	A	NP	175	3		0.019	0.0046	
5.0105	STLELRSY	10	FLU	A	NP	376	3		0.0018	0.016	
5.0103	PSRYWAIRTR	10	FLU	A	NP	382	3		0.012	0	
5.0101	RMVLSAFDER	10	FLU	A	NP	65	3		0.0014	0.010	
5.0061	FYIQMCTEL	9	FLU	A	NP	39	24				2.9
5.0060	AYERMNAIL	9	FLU	A	NP	218	24				0.031
5.0112	RFYQMCTEL	10	FLU	A	NP	38	24				0.15

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Table 23(d)

SEBID No:	Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
254	10155	LLDTASALY	9	HBV	adr	CORE	420	1	25	0.0007	0	
255	10186	SLDVSAAFY	9	HBV	adr	POL	1001	1	17.2	0.0087	0.0006	
256	20125	PTTGRTSLY	9	HBV	ALL		1382	1	1.3	0.0008	0	
257	20126	MSITDLEAY	9	HBV	adr		1521	1	0.85	<0.0008	0	
258	10208	PTTGRTSLY	9	HBV	adr	POL	1382	1	0.77	0	0	
259	10387	LTQYLNLY	9	HBV	adw	POL	1280	1	0.50	0.0003	0.0075	
260	20122	LTQYLNLY	9	HBV	adw	POL	1280	1	0.045			
261	10166	KVGNFTGLY	9	HBV	adr	POL	629	1	0.068	0.30	0.014	
262	20127	MSITDLEAY	9	HBV	adw		1550	1	0.067			
263	20120	FSQFSRGNY	9	HBV	syw		984	1	0.057			
264	20112	PSSWAFAY	9	HBV	adw		316	1	0.054			
265	20119	QSAVRKEAY	9	HBV	adw		881	1	0.025			
266	10174	PLDKGKPY	9	HBV	adr	POL	698	1	0.019	<0.0002	<0.0002	
267	10378	SLMLLYKTY	9	HBV	adw	POL	1092	1	0.017			
268	20115	ASRDLVVS	9	HBV	syw		499	1	0.013			
269	20124	PSRGRLGLY	9	HBV	adr/adw		1364	1	0.011			
270	20121	SSISRNIN	9	HBV	adr		1036	1	0.0097			
271	10519	DLDTASALY	10	HBV	adr	CORE	419	1	11.1	0	0	
272	10513	LLDPVRGLY	10	HBV	adr	ENV	120	1	6.3	0.17	0	
273	20239	LSLDVSAAPY	10	HBV	ALL		1000	1	4.2	<0.0009	0.0037	
274	10911	FLCQYLHLY	10	HBV	adr	POL	1250	1	1.1	0.014	0.0048	0.0017
275	20216	QTFGRKLHLY	10	HBV	syw	POL	1087	1	1.1	0.0056	0.012	
276	20244	KTYGRKLHLY	10	HBV	adw		1098	1	0.69	0.59	0.22	0
277	10791	KTYGRKLHLY	10	HBV	adw	POL	1098	1	0.57	0.53	0.35	0.0001
278	20242	QTFGRKLHLY	10	HBV	syw		1087	1	0.37	0.0087	0.011	
279	10556	KTFGRKLHLY	10	HBV	adr	POL	1069	1	0.34	0.094	0.090	0
280	20241	KTFGRKLHLY	10	HBV	adr		1069	1	0.30	0.15	0.095	0
281	10766	LQDFVRALY	10	HBV	adw	ENV	120	1	0.21	0.014	0	
282	10806	TTPAQGTSY	10	HBV	adw	ENV	288	1	0.20	0	0	
283	20240	LSISRNIN	10	HBV	adr		1035	1	0.20	<0.0009	0	
284	10541	PLDKGKPY	10	HBV	adr	POL	698	1	0.16	0	0	
285	20238	HSASFQSPY	10	HBV	syw		767	1	0.15	0.019	0.017	0
286	10795	FLTKQYLNLY	10	HBV	adw	POL	1279	1	0.12	0	0	
287	20237	RSASPCSPY	10	HBV	adr/adw		738	1	0.11	0.033	0.020	0
288	10774	WLWGMIDIPY	10	HBV	adw	CORE	416	1	0.081	<0.0002	<0.0002	
289	20233	TTPAQGTSY	10	HBV	syw		288	1	0.066			
290	10542	HTLWKAGILY	10	HBV	adr	POL	723	1	0.030			
291	20231	TSCPPICPY	10	HBV	adr		226	1	0.018			

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Table 23(d)
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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
20246	KSVQHLESLEY	10	HBV	adw		1,161	1	0.016			
20247	NLYVSLILLY	10	HBV	adr	POL	1059	1	0.015			
20248	LYQTEGRK	9	HBV	adw	ENV	334	2-1	0.0004	0.019	0	0.0005
20249	LYQTEGRK	9	HBV	adw	POL	1084	3		1.8	0.64	
20250	IMPAPFYK	9	HBV	adw		713	3		0.99	1.5	
20251	CLHOSPVKK	9	HBV	adw	POL	867	3		0.14	0.025	
20252	SAKSVVRR	9	HBV	adw	POL	531	3		<0.0003	0.067	
20253	HLHQDIKK	9	HBV	adw	POL	686	3		0.041	0.0075	
20254	SLPQEHQK	10	HBV	adw	POL	1197	3		0.36	4.2	
20255	SMFPSCCTK	10	HBV	adw/adw		295	3		0.43	1.9	
20256	SMYFSCCTK	10	HBV	adw		295	3		1.1	1.79	
20257	QAFISPTK	10	HBV	adw	POL	665	3		0.15	1.3	
20258	LLLYQTEGRK	10	HBV	adw	POL	1083	3		0.89	0.021	
20259	YMDVVVLGAK	10	HBV	ALL		1,123	3		0.16	0.0076	
20260	TSKSVVRR	10	HBV	adw	POL	530	3		0.0006	0.013	
20261	PTYKAFCK	9	HBV	adw	POL	1263	11		0.090	0.085	
20262	PTDLEAYK	9	HBV	adw	"X"	1552	11		0.002	0.016	
20263	KYTSPPWLL	9	HBV	ALL		1,330	24				3.6
20264	LYAAVTNKL	9	HBV	adw		1,169	24				3.2
20265	FYPNLTLY	9	HBV	adw		689	24				2.1
20266	LYSSTVPSF	9	HBV	adw/adw		665	24				1.9
20267	FYPKVTLY	9	HBV	adw		718	24				1.7
20268	FYPNVTLY	9	HBV	adw		718	24				1.6
20269	LYSLSPEL	9	HBV	adw		368	24				0.50
20270	LYSSTVPL	9	HBV	adw		636	24				0.37
20271	LYNLSPEL	9	HBV	adw		368	24				0.34
20272	NYRVSWPKE	9	HBV	adw		991	24				0.18
20273	HYPTTRHYL	9	HBV	adw/adw		743	24				0.15
20274	HYPTTRHYL	9	HBV	adw		714	24				0.057
20275	CYPALMPLY	9	HBV	ALL		1,224	24				0.049
20276	AYRPNAPF	9	HBV		NUC:NUCFUS	131	24				0.026
20277	LYQTEGRK	9	HBV	adw		1,085	24				0.014
20278	SYQHFRLL	9	HBV	adw		607	24				0.011
20279	LYSHPIGLF	10	HBV	ALL		1,077	24				1.1
20280	LYAAVTNKL	10	HBV	adw		1,169	24				0.32
20281	LYRPLSLPF	10	HBV	adw		1,371	24				0.25
20282	SYQHFRLL	10	HBV	adw		607	24				0.16
20283	SYQHFRKLL	10	HBV	adw/adw		578	24				0.066

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Table 23(d)
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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
20176	YYPEHLVNHY	10	HBV	ayw		735	24				0.040
20172	AYRPPNAPIL	10	HBV	ALL		521	24				0.022
20171	CYRWMLRRF	10	HBV	ALL		234	24				0.011
50115	NELSLGHL	10	HBV								0.0099
10377	YVSLMLLYK	9	HBV	adw	POL	572	24				
10189	LLYKTFGRK	9	HBV	adw	POL	1090	3,11		0.31	7.4	
10379	LLYKTYGRK	9	HBV	adr	POL	1066	3,11		5.0	0.30	
10370	VTKYLPDK	9	HBV	adw	POL	1095	3,11		2.5	0.40	
10176	RHYLHLWK	9	HBV	adw	POL	722	3,11		0.014	1.3	
10367	STVPSFNPK	9	HBV	adr	POL	719	3,11		1.2	0.010	
10215	TTDLAEYFK	9	HBV	adw	POL	668	3,11		0.021	0.93	
10948	YVSLLLLYK	9	HBV	adr	"X"	1523	3,11		0.0006	0.92	
10883	PTYKAFLLK	9	HBV	adw	POL	1061	3,11		0.39	0.92	
10987	HLYPVAROR	9	HBV	adr	POL	1274	3,11		0.17	0.71	
10358	STNRQLGRK	9	HBV	adw	POL	1257	3,11		0.54	0.0020	
10991	ALRFTSARR	9	HBV	adr	ENV	85	3,11		0.51	0.34	
10197	PVNRPDWK	9	HBV	adr	"X"	1488	3,11		0.44	<0.0005	
10569	TVNENRRLK	9	HBV	adw	POL	1197	3,11		0.080	0.41	
11041	VVNHVQTR	9	HBV	adw	POL	703	3,11		0.016	0.40	
10152	STTSTGPKK	9	HBV	adr	POL	740	3,11		0.080	0.33	
10213	QVLPKLLHK	9	HBV	adr	ENV	277	3,11		0.011	0.29	
10172	LTKYLPDK	9	HBV	adr	"X"	1505	3,11		0.10	0.28	
10574	CLHQSAVRK	9	HBV	adw	POL	693	3,11		0.0039	0.23	
10980	VVDFSQFSR	9	HBV	adr	POL	878	3,11		0.22	0.017	
10882	PLYACIQAK	9	HBV	adw	POL	963	3,11		0.011	0.20	
20074	YVNTNMGK	9	HBV	ayw	POL	1259	3,11		0.18	0.034	
10199	PLYACIQSK	9	HBV	adr	CORE	507	3,11		0.16	0.048	
10972	RLADEGLNR	9	HBV	adr	POL	1230	3,11		0.11	0.018	
10976	AVNHYFKTR	9	HBV	adr	POL	601	3,11		0.10	0.025	
10975	RLKLMFAR	9	HBV	adr	POL	711	3,11		0.0071	0.098	
10977	ILYKRETR	9	HBV	adr	POL	680	3,11		0.095	0.0002	
10993	KVFLGCKR	9	HBV	adr	POL	730	3,11		0.095	<0.0005	
10165	NVSIPTWK	9	HBV	adr	"X"	1548	3,11		0.042	0.082	
10982	LLYKTFGR	9	HBV	adr	POL	621	3,11		0.072	0.076	
10978	RLVRFQSTR	9	HBV	adr	POL	1065	3,11		0.072	0.0045	
10219	FVLGGRHK	9	HBV	adr	POL	757	3,11		0.068	0.0032	
11042	RLVLQSTR	9	HBV	adw	"X"	1550	3,11		0.065	0.019	
					POL	786	3,11		0.064	0.0002	

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Table 23(d)
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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.1043	MLLYKTICR	9	HBV	adw	POL	1094	3,11		0.061	0.0032	
1.1070	TVNEKRRLK	9	HBV	adr	POL	674	3,11		0.048	0.007	
1.1045	NLYPVARQR	9	HBV	adw	POL	1286	3,11		0.042	0.0011	
1.1046	LPYRPTTCR	9	HBV	adw	POL	1407	3,11		0.021	0	
1.0845	LVSRGWIR	9	HBV	adr	CORE	509	3,11		0.0033	0.020	
1.0981	LVGSSGLPR	9	HBV	adr	POL	1022	3,11		0.0008	0.015	
1.0967	HISCLITCR	9	HBV	adr	CORE	494	3,11		0.013	0.011	
1.1047	SVPSKLPDR	9	HBV	adw	POL	1424	3,11		0.0007	0.010	
1.0989	SVPSHLPDR	9	HBV	adr	POL	1395	3,11		0.0004	0.010	
1.0564	TLPOEHVLK	10	HBV	adr	POL	1179	3,11		0.092	5.6	
2.0205	TVPVNPHWK	10	HBV	ayw	POL	669	3,11		0.0067	4.2	
1.0543	TLWKAGILYK	10	HBV	adr	POL	724	3,11		3.5	1.0	
1.0807	SMYPSCCCTK	10	HBV	ayw	ENV	295	3,11		1.5	3.4	
1.1153	RLPYRPTTCR	10	HBV	adw	POL	1406	3,11		2.8	0.030	
1.0584	STTDLEAYEK	10	HBV	adr	X	1522	3,11		0.0066	2.7	
1.0554	LLLYKTICR	10	HBV	adr	POL	1065	3,11		2.5	0.012	
1.0799	TVNAHRNLPK	10	HBV	adw	X	1529	3,11		0.82	0.65	
1.0886	EATKDCLEK	10	HBV	adr	X	1527	3,11		0.007	0.74	
1.1081	LVNDSQFSR	10	HBV	adr	POL	962	3,11		0.0009	0.63	
1.0789	MLLYKTICR	10	HBV	adw	POL	1094	3,11		0.61	0.020	
1.0546	TAYSHLSTK	10	HBV	adr	POL	858	3,11		0.26	0.092	
1.0562	SLGHLNPNK	10	HBV	adr	POL	1150	3,11		0.20	0.078	
1.1152	RLGLYRPLR	10	HBV	adw	POL	1397	3,11		0.19	0.0049	
1.0547	VTCGVFLVDK	10	HBV	adr	POL	943	3,11		0.035	0.17	
1.1150	RIRTPRIPAR	10	HBV	adw	POL	962	3,11		0.17	0.0002	
1.0581	TVNGHQVLPK	10	HBV	adr	X	1500	3,11		0.073	0.092	
1.1091	SLPQPTTCR	10	HBV	adr	POL	1377	3,11		0.077	0.043	
1.1072	TLPETTVRR	10	HBV	adr	CORE	532	3,11		<0.003	0.075	
1.1089	GTDSNVLSR	10	HBV	adr	POL	1320	3,11		0.025	0.072	
1.1071	SLPETTVRR	10	HBV	adr	CORE	531	3,11		0.0005	0.068	
2.0210	KVTKYLPDK	10	HBV	ayw	POL	721	3,11		0.027	0.053	
1.1148	STRHCKSFR	10	HBV	adw	POL	792	3,11		0.0057	0.038	
1.0935	VLSGWLQFR	10	HBV	adw	POL	923	3,11		0.029	0.0087	
1.0781	NVTKYLPDK	10	HBV	adw	POL	721	3,11		<0.0004	0.023	
1.1092	RVCQQLDPAR	10	HBV	adr	X	1422	3,11		0.0019	0.023	
1.0793	SLGHLNPNK	10	HBV	adw	POL	1179	3,11		0.017	0.014	
1.0909	YLYSECVWIR	10	HBV	adr	CORE	508	3,11		0.015	0.0027	

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Table 23(d)
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SEQ ID NO:	Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
398	2.0207	FVGLTVNEK	10	HBV	ayw	POL	698	3,11		0.0057	0.015	
399	1.0535	YVGLTVNEK	10	HBV	adr	POL	669	3,11		0.0069	0.014	
400	1.1075	RLADEGLNRR	10	HBV	adr	POL	601	3,11		0.013	0.0004	
401	1.1086	IVLKLKQCFR	10	HBV	adr	POL	1185	3,11		0.013	0.0024	
402	1.0773	PIPSSWAFK	10	HBV	adw	ENV	314	3,11		<0.0003	0.010	
403	1.0778	LTVNIENRRLK	10	HBV	adw	POL	702	3,11		0.0025	0.0095	

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Table 23(e)

SEQ ID NO:	Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
404	1.0118	CTCGSSDLY	9	HCV		LORF	1123	1	3.0	0	0.010	
405	1.0112	NIVDVQYLY	9	HCV		NS1/ENV2	697	1	0.60	0	0.010	
406	2.0034	VQDCNCSY	9	HCV			302	1	0.54	0.0005	0.0003	
407	2.0035	LTPRCMVDY	9	HCV			605	1	0.078			
408	1.0145	RVCEKMALY	9	HCV		LORF	2588	1	0.053			
409	1.0140	DVVCSSMSY	9	HCV		LORF	2416	1	0.039			
410	2.0036	FTIFKIRMY	9	HCV			626	1	0.012			
411	1.0509	GLSAFSLHSY	10	HCV		LORF	2888	1	0.41	0.013	0.0034	0.0002
412	1.0489	TLHGPTPLY	10	HCV		LORF	1617	1	0.30	0.11	0.0024	
413	2.0037	EYVLLFL	9	HCV			719	24				1.4
414	2.0169	MYVGGVEHRL	10	HCV			633	24				0.026
415	2.0170	EYVLLFL	10	HCV			719	24				0.010
416	1.0139	SVPAELRK	9	HCV		LORF	2269	3,11		0.016	0.87	
417	1.0955	QLFTSPRR	9	HCV		ENV1	290	3,11		0.75	0.033	
418	1.0090	RLGVRATRK	9	HCV		CORE	43	3,11		0.74	0.16	
419	1.0123	LIFCHSKK	9	HCV		LORF	1391	3,11		0.54	0.19	
420	1.0122	HLRCHSKK	9	HCV		LORF	1390	3,11		0.25	0.010	
421	1.0952	KTISRSQPR	9	HCV		CORE	51	3,11		0.16	0.064	
422	1.0120	AVCTRGVAK	9	HCV		LORF	1183	3,11		0.016	0.038	
423	1.0143	EVRCVQPEK	9	HCV		LORF	2563	3,11		0.0019	0.033	
424	1.0137	ITRVESENK	9	HCV		LORF	2241	3,11		0.015	0.0079	
425	1.0957	CIITSLTGR	9	HCV		LORF	1042	3,11		0.0095	0.011	
426	1.0496	GVAGALVAFK	10	HCV		LORF	1858	3,11		0.87	1.1	
427	1.0480	HLHAPTCGK	10	HCV		LORF	1227	3,11		0.57	0.0051	
428	1.1062	RMVGGVEHR	10	HCV		NS1/ENV2	632	3,11		0.27	0.012	
429	1.0485	HLIFCHSKK	10	HCV		LORF	1390	3,11		0.27	0.025	
430	1.0484	TLGFGAYMSK	10	HCV		LORF	1261	3,11		0.17	0.13	
431	1.1067	GVGTYLLPNR	10	HCV		LORF	3002	3,11		0.0029	0.032	
432	1.1063	LLFLLADAR	10	HCV		NS1/ENV2	723	3,11		0.015	0	

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Table 23(f)

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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0014	FRDYVDRFY	9	HIV		GAG	298	1	0.090			
2.0129	TYQYMDLL	9	HIV			875	1	0.064			
1.0028	TVLDVGDAY	9	HIV		POL	802	1	0.018	<0.0002	0.0056	
1.0412	VTVDVGDAY	10	HIV		POL	801	1	0.28	0	0.0004	
1.0415	VYQYMDLL	10	HIV		POL	874	1	0.25	0.0007	0.0090	
2.0252	VTVDVGDAY	10	HIV			801	1	0.088			
1.0431	EVNIVDSQY	10	HIV		POL	1187	1	0.053			
1.0441	LVAHVVASGY	10	HIV		POL	1329	1	0.039			
1.0442	PAETGQETAY	10	HIV		POL	1345	1	0.013			
2.0251	ISKIGPENPY	10	HIV			742	1	0.013			
2.0255	QMAVTHNFK	10	HIV			1432	3		0.61	0.64	
2.0064	RYLKDQQL	9	HIV			2778	24				0.76
2.0134	RYLKDQQL	9	HIV			2778	24				0.32
2.0065	TYQYQEPF	9	HIV			1033	24				0.30
2.0131	TYQYQEPF	9	HIV			1033	24				0.20
2.0063	TYQYQENL	9	HIV			1036	24				0.052
2.0132	TYQYQENL	9	HIV			1036	24				0.033
2.0066	TYQYMDLL	9	HIV			875	24				0.013
2.0247	TYKRWILGL	10	HIV			266	24				0.017
2.0190	TYKRWILGL	10	HIV			266	24				0.014
2.0249	LYPLASLSL	10	HIV			506	24				0.014
1.0069	KLACRWPFVK	9	HIV		POL	1358	3,11		2.7	0.069	
1.0944	AVFHNFKR	9	HIV		POL	1434	3,11		0.17	1.8	
1.0032	AFQSMATK	9	HIV		POL	853	3,11		1.1	0.96	
1.0046	IVWCKTPK	9	HIV		POL	1075	3,11		0.085	0.37	
1.0079	KLTEDRWNK	9	HIV		VIF	1712	3,11		0.013	0.27	
1.0027	GIPHPAGLK	9	HIV		POL	788	3,11		0.23	0.865	
1.0069	QIEQLKK	9	HIV		POL	1215	3,11		0.0091	0.16	
1.0939	KIWPSYKCR	9	HIV		GAG	443	3,11		0.12	0.0005	
1.0072	ILATDQTK	9	HIV		POL	1458	3,11		0.025	0.098	
1.0036	MGYELHPOK	9	HIV		POL	925	3,11		0.064	0.096	
1.0062	YLAWVPAHK	9	HIV		POL	1227	3,11		0.077	0.057	
1.0938	KIWPSHKCR	9	HIV		GAG	443	3,11		0.077	<0.0005	
1.0047	FVNTPLVK	9	HIV		POL	1111	3,11		0.012	0.066	
1.0024	NTPVFAKK	9	HIV		POL	752	3,11		0.033	0.060	
1.0080	TVQCTHGK	9	HIV		ENV	2420	3,11		0.0021	0.046	
1.0013	ILDIRQGPVK	9	HIV		GAG	287	3,11		0.042	0.0048	

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Table 23(f)
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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0015	RDYVDRFYK	9	HIV		GAG	299	3.11		0.0007	0.040	
1.0058	GIQAQPDK	9	HIV		POL	1199	3.11		<0.0009	0.040	
1.0064	VLFLDGIDK	9	HIV		POL	1254	3.11		0.038	0.032	
1.0026	LVDFRELNK	9	HIV		POL	769	3.11		0.011	0.030	
1.0078	KVPRRKAK	9	HIV		POL	1513	3.11		0.029	0.0039	
1.0942	MTKILEPFR	9	HIV		POL	859	3.11		<0.0008	0.016	
1.0463	TVYGVVWVK	10	HIV		ENV	2185	3.11		3.8	7.8	
1.0418	TVQIVLPEK	10	HIV		POL	935	3.11		0.16	5.6	
1.0447	AVFIHFKRK	10	HIV		POL	1434	3.11		0.66	0.85	
1.0437	KVFLDGDIDK	10	HIV		POL	1253	3.11		0.36	0.78	
1.0408	KLVDRELNK	10	HIV		POL	768	3.11		0.51	0.090	
1.0403	KLKFGMDGPK	10	HIV		POL	706	3.11		0.39	0.076	
1.0395	FLGKIWFPSYK	10	HIV		GAG	440	3.11		0.32	0.024	
1.1056	KIQNFRVYR	10	HIV		POL	1474	3.11		0.032	0.21	
1.0410	GIPHPAGLKK	10	HIV		POL	788	3.11		0.011	0.17	
1.0426	LVKLWYQLEK	10	HIV		POL	1117	3.11		0.056	0.082	
1.0398	MIGGIGGFK	10	HIV		POL	642	3.11		0.0099	0.055	
1.0413	MTKILEPRK	10	HIV		POL	859	3.11		0.015	0.038	
1.0453	VVIQNSDIK	10	HIV		POL	1504	3.11		<0.0005	0.021	
1.0394	FLGKIWFPSHK	10	HIV		GAG	440	3.11		0.020	0.0013	
1.1059	IVQQNNLLR	10	HIV		ENV	2741	3.11		0.0024	0.019	
1.0417	FTTPDKKHQK	10	HIV		POL	909	3.11		<0.0002	0.015	
1.0405	LVEICTEMEK	10	HIV		POL	729	3.11		0.0002	0.012	
1.0392	LVQNANPDCK	10	HIV		GAG	327	3.11		<0.0002	0.011	

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Table 23(g)

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0225	ISEYRHYCY	9	HPV	16	E6	80	1	7.8	0.0011	0.036	
1.0230	QAEPRDRAHY	9	HPV	16	E7	44	1	0.021	<0.0002	<0.0002	
1.0610	LODIEITCVY	10	HPV	18	E6	25	1	0.25	0.0056	0.012	
2.0159	YSKISEYRHY	10	HPV	16	E6	77	1	0.17	<0.0009	0	
2.0162	YSKISEYRHY	10	HPV	16	E6	77	1	0.11	<0.0009	0	
1.0599	HGDTPTLHEY	10	HPV	16	E7	2	1	0.087	<0.0002	<0.0002	
1.0601	QPETDOLYCY	10	HPV	16	E7	16	1	0.033			
1.0913	IHDILCEVY	10	HPV	16	E6	30	1	0.032			
1.0594	AVCDKCLKFY	10	HPV	16	E6	68	1	0.0095	0.0052	0.019	
2.0160	YSRRELRYHY	10	HPV	18	E6	72	1	0.018	<0.0002	<0.0002	
2.0164	YSRRELRYHY	10	HPV	18	E6	72	1	0.012			
2.0161	LLRLCLRCQK	10	HPV	18	E6	101	3		0.001	0.078	
2.0032	HTMLCMCK	9	HPV	18	E7	59	11		0.020	0.079	0.33
2.0029	VYCKTVLEL	9	HPV	18	E6	33	24				0.057
2.0027	CYSLYGITL	9	HPV	16	E6	87	24				0.032
2.0024	VYDFAPRDL	9	HPV	16	E6	49	24				0.019
2.0031	LYNLLRLCL	9	HPV	18	E6	98	24				0.010
2.0030	VYGDITLEKL	9	HPV	18	E6	85	24				
1.0239	SVYGDITLEK	9	HPV	18	E6	84	3,11		0.39	2.3	
1.0243	SVYGDITLEK	9	HPV	18	E6	84	3,11		0.55	1.1	
1.0244	SVYGDITLEK	9	HPV	18	E6	84	3,11		0.70	0.95	
1.0226	TLLEQQYNK	9	HPV	16	E6	93	3,11		0.010	0.67	
1.0241	SIPHAACHK	9	HPV	18	E6	59	3,11		0.0094	0.25	
1.0237	SIPHAACHK	9	HPV	18	E6	59	3,11		0.017	0.12	
1.0233	IVCPICQK	9	HPV	16	E7	89	3,11		0.035	0.023	
1.0997	KLRLHNEKR	9	HPV	18	E6	117	3,11		0.025	<0.0005	
1.0234	LLRLCLRCQK	9	HPV	18	E6	102	3,11		0.019	0.0012	
1.0853	ILLECVYCK	9	HPV	16	E6	33	3,11		0.0016	0.019	
1.0999	CIDFYSRUR	9	HPV	18	E6	68	3,11		0.017	0.0018	
1.0998	CIDFYSRUR	9	HPV	18	E6	68	3,11		0.010	0.0009	
1.0596	GITLEQQYNK	10	HPV	16	E6	92	3,11		0.010	0.98	
1.0606	LLRLCLRCQK	10	HPV	18	E6	101	3,11		0.076	0.29	
1.0598	LLRLCLRCQK	10	HPV	16	E6	106	3,11		0.12	0.24	
1.0629	LLRLCLRCQK	10	HPV	18	E6	101	3,11		0.16	0.11	
1.0614	LTEVEFAFK	10	HPV	18	E6	41	3,11		0.0009	0.11	
1.0605	GIVCPICQK	10	HPV	16	E7	88	3,11		0.0017	0.060	
1.0625	LTEVEFAFK	10	HPV	18	E6	41	3,11		0.0012	0.041	
1.0591	DIILECVYCK	10	HPV	16	E6	32	3,11		0.0065	0.021	
1.1101	KLRLHNEKR	10	HPV	18	E6	117	3,11		0.013	0	
1.1095	CVYCKQQLLR	10	HPV	16	E6	37	3,11		0.011	0.0059	

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Table 23(h)

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
20020	EVDPIGHLY	9	MAGE	3		161	1	18	0.0002	0.0009	
30172	EADPTSTNY	9	MAGE	5/51		161	1	9.9	0.0006	0.0006	0
10258	LTQDLVQEKY	9	MAGE	1		240	1	2.1	0	0.0002	
30173	EVDPTGHVY	9	MAGE	6		161	1	1.9	<0.0002	<0.0002	0
10254	EADPTGHVY	9	MAGE	1		161	1	1.1	0	0	
10259	LVQKLTLEY	9	MAGE	1		243	1	0.42	0.0013	0.053	
60053	TSYKVLLEY	9	MAGE	1	new	275	1	0.099			
20009	SLPTTTHNY	9	MAGE	3		9	1	0.055			
20011	GSMGNWQY	9	MAGE	3		77	1	0.050			
20008	SPSTTHNY	9	MAGE	2		9	1	0.043			
10252	MLESVDNY	9	MAGE	1		128	1	0.011			
20147	ASSLPTTHNY	10	MAGE	3		8	1	2.6	<0.0009	0.053	
20167	LTQDLVQEKY	10	MAGE	1		239	1	1.2	<0.0009	0.0073	
60114	EISTYKVLLEY	10	MAGE	1	new	274	1	0.56			
20141	ASSSTTHNY	10	MAGE	2		8	1	0.17	<0.0009	0.026	
10648	DLVQKLTLEY	10	MAGE	1		242	1	0.044			
60045	TSYKVLLEY	9	MAGE	1	new	275	3		0.71	0.010	
40119	TITNPTQR	9	MAGE	1		66	3		0.043	0.37	
60044	ALAEISYK	9	MAGE	1		271	3		0.31	0.36	
40132	LTQDLVQEKY	9	MAGE	1	new	239	3		<0.0003	0.14	
60062	LVQKLTLEY	9	MAGE	1	new	243	3		0.026	0.034	
40131	HSAYCEPRK	9	MAGE	1		229	3		0.074	0.0009	
40122	LPRAVITK	9	MAGE	1		97	3		0.011	0.0005	
60124	RYRHHFSLR	10	MAGE	1		290	3		0.43	0.0009	
40161	ADLVGRLLK	10	MAGE	1		107	3		0.35	0.29	
40160	ESLRAVITK	10	MAGE	1		95	3		0.14	0.068	
60119	DLVQKLTLEY	10	MAGE	1	new	242	3		0.032	0.051	
60123	YVKSASRYK	10	MAGE	1	new	283	3		0.019	0.0009	
40168	LSYMEVTDGR	10	MAGE	1		218	3		<0.0003	0.072	
40163	KAEMLSEYK	10	MAGE	1		125	3		<0.0003	0.0097	
60125	PALAEISYK	10	MAGE	1	new	270	11		0.18	0.24	
20010	NYTLWSQSY	9	MAGE	3		16	24				0.027
20165	NYKHCFPRP	10	MAGE	1		135	24				0.25
20151	LYEATCLG	10	MAGE	3		115	24				0.046
60126	SYVKLTLYI	10	MAGE	1	new	276	24				0.036
10248	SLRAVITK	9	MAGE	1		96	3,11		4.1	2.7	
10006	SYMEVTDGR	9	MAGE	1		219	3,11		0.0098	1.3	
10004	TITNPTQR	9	MAGE	1		66	3,11		0.076	1.0	
10257	LTQDLVQEKY	9	MAGE	1		229	3,11		0.0002	0.38	
10634	SLRAVITK	10	MAGE	1		96	3,11		1.2	0.98	
10647	LTQDLVQEKY	10	MAGE	1		238	3,11		0.0004	0.16	
10640	MLESVDNYK	10	MAGE	1		128	3,11		0.14	0.027	
10644	LLCQNGIMPK	10	MAGE	1/3		182	3,11		0.020	0.071	
10630	SLFQSLHCK	10	MAGE	1		2	3,11		0.015	0.015	

SEQ ID

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Version with markings to show changes made

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Table 23(i)

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0281	GSDCTTHY	9	p53			226	1	29.5	0.0010	0.029	
1.0667	GTAKSVICTY	10	p53			117	1	0.33	0.023	0.049	0
1.0672	RVEGNLRVEY	10	p53			196	1	0.022	0.0014	0.0020	
1.0278	RVRAMATYK	9	p53			156	3,11		1.5	0.73	
1.0276	CTYSPALNK	9	p53			124	3,11		0.46	1.1	
1.0285	NTSSSPQPK	9	p53			311	3,11		0.0009	0.095	
1.0284	RTEENLRK	9	p53			283	3,11		0.0015	0.091	
1.0287	ELNEALELK	9	p53			343	3,11		0.020	0.0052	
1.0678	RTEENLRKK	10	p53			283	3,11		3.3	0.0080	
1.1113	KTYQCSYGR	10	p53			101	3,11		2.6	0.88	
1.1115	VVRCFPIHER	10	p53			172	3,11		0.099	0.0017	
1.0679	NTSSSPQPKK	10	p53			311	3,11		0.0085	0.054	
1.1121	RVCACPGRDR	10	p53			273	3,11		0.014	0.011	
1.1116	GLAPPQHLR	10	p53			187	3,11		0.013	0.0006	

Table 23(j)

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
3.0175	KGEYFVEMY	9	PAP			322	1	3.4	<0.0002	0.0002	0
3.0174	LGEYRKRY	9	PAP			81	1	0.78	<0.0002	0.0002	0
3.0166	ASCHLTLY	9	PAP			311	1	0.77	<0.0002	0.055	0
3.0163	ESYKHEQVY	9	PAP			95	1	0.098	<0.0002	0.0002	0
3.0237	LSELSLSLY	10	PAP			238	1	14	0.0026	0.0004	0
3.0235	LSELSLSLY	10	PAP			238	1	12	0.0005	0.0004	0
3.0236	LTQLGMEQHY	10	PAP			70	1	0.62	0.015	0.0024	0.0022
3.0238	KGEYFVEMY	10	PAP			322	1	0.018	0.0057	0.089	
3.0230	LVNEILNHMK	10	PAP			263	3		0.056	0.12	
3.0158	ATQPSYKK	9	PAP			274	11		0.10	1.2	
3.0231	ETLKSEEROK	10	PAP			170	11		<0.0004	0.014	
3.0161	LYFEKGEYF	9	PAP			318	24				2.5
3.0160	LYCESVHNF	9	PAP			213	24				0.44
3.0159	PKDFIATL	9	PAP			183	24				0.11
3.0162	VYNGLLPPY	9	PAP			302	24				0.032
3.0232	PYASCHLTTEL	10	PAP			309	24				0.024

added

SEQ ID
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Version with markings to show changes made

Table 23(k)

Peptide	Sequence	(SEQ ID NO.)	AA	Virus	Strain	Molecule	Pos. Motif	A1	A3.2	A11	A24
1.0270	ALPERIPSLY	(587)	9	PSA			231 1	0.011			
2.0157	VSHSPFHPLY	(588)	10	PSA			88 1	0.15	<0.0003	0.0015	
1.0265	PLYDMSLLK	(589)	9	PSA			95 3.11		0.24	0.037	
1.0273	VVHYRKWK	(590)	9	PSA			242 3.11		0.0072	0.093	
1.0272	YTKVVHYRK	(591)	9	PSA			239 3.11		0.0006	0.068	
1.1009	SLIGNRFLR	(592)	9	PSA			100 3.11		0.0024	0.047	
1.0260	IVGQWBECK	(593)	9	PSA			21 3.11		0.041	0.019	
1.0269	QVHPQKVTK	(594)	9	PSA			182 3.11		0.0060	0.014	
1.1112	SLYTKVVHYR	(595)	10	PSA			237 3.11		0.28	0.23	
1.0683	LTAAHGRNK	(596)	10	PSA			57 3.11		0.14	0.083	
1.0651	RIVGQWBECK	(597)	10	PSA			20 3.11		0.046	0.067	
1.0662	KVVHYRKWK	(598)	10	PSA			241 3.11		0.045	0.045	
1.1111	VTKFMLCAGR	(599)	10	PSA			188 3.11		0.0003	0.012	
3.0108	MLLRLSEPA	(600)	9	PSA			118 Random				

added

TABLE 24: CTL EPITOPES IDENTIFIED IN PEPTIDE SCREENING.

SEQ ID NO:

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Sequence	Antigen	Motif	Id
EVDPIGHLY	MAGE3	A01	1044.07
ASSLPPTMNY	MAGE3	A01	1044.01
EADPTGHSY	MAGE1	A01	958.01
SSLPPTMNY*	MAGE3	A01	1072.02*
GSVVGNWQY*	MAGE3	A01	1072.03*
ALAETSYVK*	MAGE1N	A03	1072.38*
SLFRAVITK	MAGE1	A11	1072.13
RALAETSYVK	MAGE1N	A11	1072.39
ESLFRAVITK	MAGE1	A11	1072.15
KVYLAWVPAHK	HIV	A3/11*	1069.42*
TVYYGVPVWK	HIV	A03	1069.43
KLGRWPVK	HIV	A03	1069.44
KMIGGIGGFIK	HIV	A03	1069.45
AIFQSSMTK	HIV	A03	966.01
WTYQIYQEPFK	HIV	A03	1069.46
FLGKIWPSHK*	HIV	A03	1069.56*
TVYYGVPVWK	HIV	A11	1052.03
VTVYYGVPVWK	HIV	A11	1069.47
GVAGALVAFK	HCV	A03	1073.10
CTCGSSDLY	HCV	A11	1069.62
GVAGALVAFK	HCV	A11	1052.05
LLDTASALY*	HBV	A01	1069.01*
TLWKAGILYK	HBV	A03	1069.15

* borderline positive

added

Version with markings to show changes made

Table 25 a

Peptides Synthesized
by Cytel For Loading
Onto Acid Stripped

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Autologous PBMCs and
PHA Blasts

Peptide ID #	Antigen	(SEQ ID NO:)	Sequence
777.03	HBs	(606)	FLLTRILTI
10 924.07	HBc	(607)	FLPSDFFPSV
927.32	HBp	(608)	GLYSSTVPV
938.01	MAGE 1	(523)	EADPTGHSY
939.03	PSA	(609)	VLVHPQWVL
941.01	HBc	(610)	FLPSDYFPSV
15 1044.04	PAP	(611)	ILLWDPIPV
1044.05	PSA	(612)	KLQCVDLVHI
1044.06	PSA	(613)	MLLRLSEPAEL

added

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Table 25 b

Cell Population

¹²⁵I-Labeled

CPMS

Peptide +/- Cold

+/- std. dev.

Peptide

JY acid stripped	- cold peptide	3553 ± 157	n = 3
25 JY acid stripped	+ cold peptide	13	n = 1
JY control	-cold peptide	370 ± 37	n = 3
JY control	+ cold peptide	50	n = 1

TABLE 13

VALIDATION OF CYTEL'S HLA MOTIFS

5	Binding Capacity (IC ₅₀ nM)						
	Sequence	Motif	A1	A2.1	A3.2	A11	A24
	AADKAAAAAY	A1	50	--*	--	--	--
	ATAKAAAAAY	A1	15	--	329	77	--
	ATDKAAAAAY	A1	2.8	--	9250	840	ND
10	ALAKAAAAV	A2.1	--	125	--	--	--
	AMAAAAAAK	A3.2	--	--	48	8.4	--
	ATAAAAAAK	A11	--	--	59	40	--
	AYAKAAAAF	A24	--	--	--	--	115

15 *A dash indicates an IC₅₀ greater than 20,000 nM.

TABLE 14

VALIDATION OF CYTEL'S HLA MOTIFS

20	Binding Capacity (IC ₅₀ nM)					
	SEQUENCE	MOTIF	A1	A2.1	A3.2	A11
	AADKAAAAAY	A1	45	---	--	--
25	ATAKAAAAAY	A1	58	--	1100	1030
	ATDKAAAAAY	A1	4.0	--	10000	4533
	ALAKAAAAV	A2.1	ND	1400	--	--
	AMAAAAAAK	A3.2	ND	--	85	24.0
	ATAAAAAAK	A11	--	--	216	88

30 *A dash indicates an IC₅₀ greater than 20,000 nM.

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TABLE 15

HLA-A3.2

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 952.25	SUBSTITUTION
	952.25	ALAAAAAAK	1	-
	952.26	AMAAAAAAK	1.2	position 2
	952.23	AVAAAAAAK	0.95	
	981.04	ASAAAAAAK	0.89	
10	952.24	AIAAAAAAK	0.57	
	952.27	AAAAAAAK	0.57	
	981.06	ATAAAAAAK	0.49	
	981.08	AFAAAAAAK	0.13	
	981.09	AGAAAAAAK	0.077	
15	981.13	ACAAAAAAK	0.031	
	981.12	ADAAAAAAK	0.014	
	981.11	ANAAAAAAK	0.0010	
	981.05	AKAAAAAAK	<0.0016	
	981.07	AYAAAAAAK	<0.0005	
20	981.10	APAAAAAAK	<0.0006	
	952.35	ALAAAAAAR	0.46	position 9
	981.36	ALAAAAAAY	0.15	
	981.33	ALAAAAAAA	0.0034	
	981.35	ALAAAAAAQ	<0.0006	
25	981.37	ALAAAAAAS	<0.0005	
	981.38	ALAAAAAAT	<0.0005	
	981.34	ALAAAAAAN	<0.0005	
	981.39	ALAAAAAAE	<0.0003	

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TABLE 16

HLA-A11

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 952.25	SUBSTITUTION
	952.25	ALAAAAAAK	1	-
	952.26	AMAAAAAAK	2.5	position 2
	952.27	AAAAAAAK	1.1	
	952.24	ALAAAAAAK	0.72	
10	981.06	ATAAAAAK	0.55	
	981.04	ASAAAAAAK	0.46	
	981.09	AGAAAAAAK	0.38	
	952.23	AVAAAAAAK	0.23	
	981.11	ANAAAAAAK	0.23	
15	981.13	ACAAAAAAK	0.019	
	981.08	AFAAAAAAK	0.020	
	981.12	ADAAAAAAK	0.012	
	981.05	AKAAAAAAK	0.0065	
	981.07	AYAAAAAAK	<0.0065	
20	981.10	APAAAAAAK	<0.0051	
	952.35	ALAAAAAAR	0.015	position 9
	981.33	ALAAAAAAA	<0.0059	
	981.34	ALAAAAAAN	<0.0071	
	981.35	ALAAAAAAQ	<0.0051	
25	981.36	ALAAAAAAY	<0.0071	
	981.37	ALAAAAAAS	<0.0051	
	981.38	ALAAAAAAT	<0.0051	
	981.39	ALAAAAAAE	<0.0071	

TABLE 17

HLA-A24

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 983.01	SUBSTITUTION
	983.01	AYAKAAAF	1	-
10	983.08	AFAKAAAF	0.24	position 2
	983.09	APAKAAAF	0.0058	
	983.10	AAAKAAAF	0.0023	
	983.11	AKAKAAAF	<0.0012	
	983.05	AYAKAAAI	0.20	position 9
15	983.04	AYAKAAAL	0.11	
	983.06	AYAKAAAV	0.0023	
	983.02	AYAKAAAA	<0.0012	
	983.03	AYAKAAAY	<0.0012	
	983.07	AYAKAAAK	<0.0012	

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TABLE 18

HLA-A1

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 982.07	SUBSTITUTION
	982.011	ATDKAAAAAY	Motif	-
	982.07	ATAKAAAAAY	1	-
	982.09	ASAKAAAAAY	0.17	position 2
	982.13	AMAKAAAAAY	0.095	no D in pos 3
10	982.08	AAAKAAAAAY	0.0064	
	954.09	ALAKAAAAAY	0.0045	
	954.11	AIAKAAAAAY	0.0045	
	954.13	AVAKAAAAAY	0.0020	
	982.10	AKAKAAAAAY	0.0011	
15	982.11	ANAKAAAAAY	<0.0001	
	982.12	ADAKAAAAAY	<0.0001	
	982.14	AGAKAAAAAY	<0.0001	
	982.15	APAKAAAAAY	<0.0001	
	982.16	AYAKAAAAAY	<0.0001	
20	982.17	AHAKAAAAAY	<0.0001	
	982.24	ATAKAAAAA	0.0040	position 9
	982.23	ATAKAAAAF	0.0019	no D in pos 3
	982.28	ATAKAAAAH	0.0010	
	982.32	ATAKAAAAV	0.0005	
25	982.25	ATAKAAAAN	<0.0001	
	982.26	ATAKAAAAD	<0.0001	
	982.27	ATAKAAAAW	<0.0001	
	982.30	ATAKAAAAK	<0.0001	
	982.31	ATAKAAAAI	<0.0001	
30	982.29	ATAKAAAAP	<0.0001	

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TABLE 19

HLA-A1

5	PEPTIDE	SEQUENCE	AVERAGE RATIO TO 982.07	SUBSTITUTION
	982.01	ATDKAAAAAY	Motif	-
	982.07	ATAKAAAAAY	1	-
	982.01	AADKAAAAAY	0.14	position 3
	954.03	AAEKAAAAAY	0.038	no T in pos 2
10	982.02	AAAKAAAAAY	0.0055	
	982.06	AASKAAAAAY	0.0024	
	982.04	AANKAAAAAY	0.0011	
	982.03	AAQKAAAAAY	0.0008	
	982.05	AAKKAAAAAY	<0.0001	
15	982.20	AADKAAAAA	0.0016	position 9
	982.21	AADKAAAAW	0.0005	no T in pos 2
	982.19	AADKAAAF	<0.0001	
	982.22	AADKAAAK	<0.0001	

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TABLE 20 (A)

HPV16 E6 AND E7 PEPTIDES BINDING TO HLA-A1

5	Origin	First aa Position	Sequence*	Binding Ratio to Standard†	Motif Prediction
10	E6	80	ISEYRHYAY	3.500	+
	E6	69	VADKALKFY	0.240	+
	E7	44	QAEPDRAHY	0.029	+
	E7	37	EIDGPAGQA	0.025	-
	E7	19	TTDLYAYEQ	0.023	+
	E6	144	MSAARSSRT	0.019	+/-
	E7	73	HVDIRTLED	0.014	-
	E6	139	WTGRAMSAA	0.010	-
15	E6	61	YRDGNPYAV	0.008	-

* Bold A's indicate residues in which cysteine was replaced by alanine.

† The average IC_{50} value \pm SE of the standard in the course of the experiments considered in this table was 81 ± 30 nM. Listed in the table are peptides yielding ratio values of ≥ 0.001 . All other peptides yielded ratio values of ≤ 0.001 .

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TABLE 20(B)
HPV16 E6 and E7 Peptides Binding to HLA-A3.2

	Origin	First aa Position	Sequence*	Binding Ratio to Standard†	Motif Prediction
5	E6	107	LIRAINAQK	3.7000	+
	E6	59	IVYRDGNFY	3.0000	+
	E7	89	IVAPIASQK	2.2000	+
10	E6	33	IILEAVYAK	1.5000	+
	E6	125	HLDKKQRFH	0.4400	+
	E6	143	AMSAARSSR	0.1800	+
	E6	7	AMFQDPQER	0.1000	+
	E6	93	TTLEQQYNK	0.0780	+
15	E6	37	AVYAKQQLL	0.0320	-
	E7	51	HYNIVTFAA	0.0210	-
	E6	145	SAARSSRTR	0.0200	+
	E6	75	KFYISKISEY	0.0100	+
	E6	89	SLYGTTLQ	0.0080	-
20	E7	52	YNIVTFAAK	0.0067	-
	E6	80	ISEYRHYAY	0.0064	+
	E6	42	QQLLRREVV	0.0058	-
	E6	68	AVADKALKF	0.0056	+
	E6	97	QQYNKPLAD	0.0045	-
25	E6	79	KISEYRHYA	0.0044	-
	E6	84	RHYAYSLYG	0.0036	-
	E6	69	VADKALKFY	0.0025	+
	E6	146	AARSSRTRR	0.0020	+
	E7	58	AAKADSTLR	0.0016	+
30	E6	38	VYAKQQLLR	0.0012	-
	E6	67	YAVADKALK	0.0012	+
	E7	60	KADSTLRLA	0.0012	-

* Bold A's indicate residues in which cysteine was replaced by alanine.

† The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 30±3 nM. Listed in the table are peptides yielding ratio value of ≥0.001. All other peptides yielded ratio values of <0.001.

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Table 20 (C)
HPV16 E6 and E7 Peptides Binding to HLA-A11.2

	Origin	First aa Position	Sequence*	Binding Ratio to Standard†	Motif Prediction
5	E6	33	IILEAVYAK	6.7000	+
	E6	93	TTLEQQYNK	1.8000	+
	E7	89	IVAPIASQK	1.3000	+
10	E6	7	AMFQDPQER	0.8400	+/-
	E6	59	IVYRDGNPY	0.4700	- (+) §
	E6	80	ISEYRHYAY	0.4300	- (+) §
	E6	37	AVYAKQQLL	0.0450	-
	E6	145	SAARSSRTR	0.0330	+/-
15	E6	107	LIRAINAQK	0.0120	+
	E7	58	AAKADSTLR	0.0110	+/-
	E6	42	QQLLRREVV	0.0084	+/- (+) §
	E6	143	AMSAARSSR	0.0084	-
	E6	79	KISEYRHYA	0.0076	-
20	E6	67	YAVADKALK	0.0074	+
	E7	52	YNIVTFAAK	0.0060	+
	E6	68	AVADKALKF	0.0037	-
	E6	69	VADKALKFY	0.0030	- (+) §
	E6	38	VYAKQQLLR	0.0022	+/-
25	E6	140	TGRAMSAAR	0.0012	+/-
	E7	90	VAPIASQKP	0.0012	-
	E7	51	HYNIVTFAA	0.0010	-

* Bold A's indicate residues in which cysteine was replaced by alanine.

† The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 10±3 nM. Listed in the table are peptides yielding ratio value of ≥0.001. All other peptides yielded ratio values of <0.001.

§ Brackets indicate score according to adjusted motif.

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Table 20(D)
HPV16 E6 and E7 Peptides Binding to HLA-A24

5	Origin	First aa Position	Sequence*	Binding Ratio to Standard†	Motif Prediction
	E6	87	AYS LY GTTL	0.1200	+
	E6	72	KALKFY SKI	0.1100	- (+) §
	E6	131	RFHNIRGRW	0.1000	+
10	E7	49	RAHYNIVTF	0.0670	- (+) §
	E6	49	VYDFAFRDL	0.0610	+
	E6	82	EYRHYAYSL	0.0460	+
	E6	26	LQTTIHDI I	0.0200	-
	E6	66	PYAVADKAL	0.0055	-
15	E6	1	MHQKRTAMF	0.0049	-
	E6	85	HYAYS LY GT	0.0037	-
	E6	44	LLRRE VY DF	0.0023	+
	E6	38	VYAKQQLLR	0.0011	-

* Bold A's indicate residues in which cysteine was replaced by alanine.
† The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 22±6 nM. Listed in the table are peptides yielding ratio value of ≥0.001. All other peptides yielded ratio values of ≤0.001.
§ Brackets indicate score according to adjusted motif.

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pub
Bio

For HLA-A11 (A*1101):

- 1 XTXXXXXXXK
- 2 XTXXXXXXXXK
- 3 XVXXXXXXXK
- 4 XVXXXXXXXXK

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For HLA-A24.1 (A*2401):

- 1 XYXXXXXXXF
- 2 XYXXXXXXXF
- 3 XYXXXXXXL
- 4 XYXXXXXXL

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Peptides with MHC Class I Binding Motifs Table 9

006T60" 0T559960

AA Position	Sequence	Antigen	HLA molecule
5	30 IHDIILECVY	HPV16.E6	A1
	69 VCDKCLKFY	HPV16.E6	A1
	77 YSKISEYRHY	HPV16.E6	A1
	80 ISEYRHYCY	HPV16.E6	A1
	92 GTTLEQQYNK	HPV16.E6	A11
	93 TTLEQQYNK	HPV16.E6	A11
10	106 LLIRCINCQK	HPV16.E6	A3
	2 HGDTPTLHEY	HPV16.E7	A1
	16 QPETTDLYCY	HPV16.E7	A1
	44 QAEPDRAHY	HPV16.E7	A1
15	89 IVCPICSQK	HPV16.E7	A3, A11
	3 RFEDPTRRPY	HPV18.E6	A1
	4 FEDPTRRPY	HPV18.E6	A1
20	25 LQDIEITCVY	HPV18.E6	A1
	41 LTEVFEFAPK	HPV18.E6	A11
	72 YSRIRELRHY	HPV18.E6	A1
	84 SVYGDITLEK	HPV18.E6	A3, A11
	101 LLIRCLRCQK	HPV18.E6	A3
25	59 HTMLCMCKK	HPV18.E7	A11

Human Papilloma Virus 16 and 18 (E6 and E7 Proteins)

006T60-0T55960
0965510-091900

Peptides with MHC Class I Binding Motifs Table 10

AA Position	Sequence	Antigen	HLA molecule
5	2 SLEQRSLHCK	MAGE 1	A3
	96 SLFRAVITK	MAGE 1	A3
	96 SLFRAVITKK	MAGE 1	A3
	108 DLVGFLLLK	MAGE 1	A3
	128 MLESVIKNIK	MAGE 1	A3
10	128 MLESVIKNY	MAGE 1	A1
	152 QLVFGIDVK	MAGE 1	A3
	161 EADPTGHSY	MAGE 1	A1
	182 LLGDNQIMPK	MAGE 1	A3
	215 WEELSVMEVY	MAGE 1	A1
15	223 VYDGREHSAY	MAGE 1	A1
	238 LLTQDLVQEK	MAGE 1	A3
	239 LTQDLVQEK	MAGE 1	A11
	239 LTQDLVQEKY	MAGE 1	A1
20	240 TQDLVQEKY	MAGE 1	A1

Melanoma Antigen MAGE 1

006T60-0T559960

Peptides with MHC Class I Binding Motifs Table 11

AA Position	Sequence	Antigen	HLA molecule
5	21 IVGGWECEK	PSA	A3, A11
	57 LTAAHCIRNK	PSA	A11
	88 VSHSFPHPPLY	PSA	A1
	95 PLYDMSLLK	PSA	A3
	178 DVCAQVHPQK	PSA	A3, A11
10	182 QVHPQKVTK	PSA	A3, A11
	236 PSLYTKVVHY	PSA	A1
	239 YTKVVHYRK	PSA	A11
	241 KVVHYRKWIK	PSA	A3, A11
	242 VVHYRKWIK	PSA	A3, A11

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Prostate Specific Antigen (PSA)

006T60-0T559960

Peptides with MHC Class I Binding Motifs Table 12

AA Position	Sequence	Antigen	HLA molecule
5	2 STNPKPQRK	HCV	A11
	14 NTNRRPQDVK	HCV	A11
	43 RLGVRATRK	HCV	A3
	302 VQDCNCSIY	HCV	A1
	556 WMNSTGFTK	HCV	A3
10	605 LTPRCMVDY	HCV	A1
	626 FTIFKIRMY	HCV	A1

Hepatitis C Virus (Consensus Sequence)

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006T60" 091900

Avul.
BLZ

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006F60" 0T559960

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0300	HLDMLRHLY	9	c-EB2			42	1	9.1	0.037	0.0032	
1.0346	LLDDIDETV	9	c-EB2			849	1	7.8	0.0003	0	
1.0305	GTQLFEDNY	9	c-EB2			104	1	0.18	0	0.028	
1.0363	LTCSPQEV	9	c-EB2			1131	1	0.13	0	0.0061	
1.0317	ETLEETCV	9	c-EB2			401	1	0.043			
1.0749	PTHQSDVWVY	10	c-EB2			899	1	2.7	0.0003	0.0005	
1.0747	RLDDIDETV	10	c-EB2			868	1	1.3	0.0017	0	
1.0715	TLEETGELY	10	c-EB2			402	1	1.1	0	0	
1.0737	YVMAGVQSPY	10	c-EB2			772	1	1.1	0.018	0.012	0
1.0764	GTPTAENPEY	10	c-EB2			1239	1	0.063			
1.0705	LQRPOLCY	10	c-EB2			154	1	0.030			
1.0693	VVQCNLELY	10	c-EB2			55	1	0.018			
1.0754	MGDLVDAEY	10	c-EB2			1014	1	0.012			
1.1028	KIRKYTMRR	9	c-EB2			681	3.11		0.76	0.0018	
1.1027	VVPGILIKR	9	c-EB2			649	3.11		0.11	0.72	
1.0344	LVKSPNHVK	9	c-EB2			832	3.11		0.48	0.070	
1.0305	VLRENTSPK	9	c-EB2			754	3.11		0.40	0.013	
1.0329	ILIKRRQOK	9	c-EB2			673	3.11		0.38	0.0097	
1.0311	ILWKDIFHK	9	c-EB2			167	3.11		0.28	0.31	
1.1033	KITDGLAK	9	c-EB2			860	3.11		0.17	0.34	
1.0849	GVVPGILIK	9	c-EB2			648	3.11		0.0047	0.089	
1.0299	QVCTGTDMK	9	c-EB2			24	3.11		0.0007	0.052	
1.1081	LLDHVRENR	9	c-EB2			806	3.11		0.037	<0.0006	
1.1026	CYNCSQFLR	9	c-EB2			538	3.11		0.0015	0.031	
1.1023	TVCAGCCAR	9	c-EB2			218	3.11		0.0004	0.023	
1.0331	ILKETELRK	9	c-EB2			714	3.11		0.019	0.0023	
1.1024	VTAEQGTOR	9	c-EB2			322	3.11		<0.0002	0.014	
1.0326	OLSYMPWK	9	c-EB2			607	3.11		0.0005	0.010	
1.0707	TILWKDIFHK	10	c-EB2			166	3.11		0.043	3.6	
1.0712	GTQRCCKCSK	10	c-EB2			327	3.11		0.021	0.61	
1.0736	KVLRENTSPK	10	c-EB2			753	3.11		0.38	0.22	
1.0702	QLRSLTELK	10	c-EB2			141	3.11		0.20	0.013	
1.1142	RLVHRDLAAR	10	c-EB2			840	3.11		0.18	0	
1.0741	LLNWQMLAK	10	c-EB2			822	3.11		0.14	0.14	
1.0752	TIDVYMDIVK	10	c-EB2			948	3.11		0.013	0.12	
1.0731	RLKETELRK	10	c-EB2			713	3.11		0.057	0.11	
1.0745	VLKSPNHVK	10	c-EB2			851	3.11		0.082	0.0072	
1.1131	SVFQNLQVIR	10	c-EB2			423	3.11		0.017	0.075	
1.1133	HTVPWDQLFR	10	c-EB2			478	3.11		0.0035	0.072	
1.1127	ILKGCVLQIR	10	c-EB2			148	3.11		0.040	0.0005	
1.1143	LVSEPSRMAR	10	c-EB2			972	3.11		0.0072	0.033	
1.1136	GVVPGILIKR	10	c-EB2			648	3.11		0.018	0.033	
1.0726	CVARCPGVK	10	c-EB2			596	3.11		0.022	0.0042	
1.1137	VVPGILIKR	10	c-EB2			649	3.11		0.0030	0.016	
1.0728	GLIKRRQOK	10	c-EB2			672	3.11		0.015	0.0014	
1.1129	RTVCAGCCAR	10	c-EB2			217	3.11		0.0048	0.013	
1.1134	GLACHQLCAR	10	c-EB2			508	3.11		0.011	0	
1.1139	KIPVAIKVLR	10	c-EB2			747	3.11		0.0008	0.0099	

Table 23(a)

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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos. Motif	A1	A3.2	A11	A24
1.0291	VCEADYFEY	9	EBNA1			409 1	0.016			
1.0295	PLRESIVCY	9	EBNA1			553 1	0.010			
1.0681	PVCEADYFEY	10	EBNA1			408 1	0.015			
1.0683	CTWVAGVPVY	10	EBNA1			501 1	0.014			
1.0293	GVPVYCCSK	9	EBNA1			506 3.11		0.30	0.61	
1.1016	KTSLYNLK	9	EBNA1			514 3.11		0.31	0.12	
1.0297	AIKDLVMTK	9	EBNA1			578 3.11		0.048	0.034	
1.0687	QTHIFAELK	10	EBNA1			547 3.11		0.010	0.21	
1.1124	CTALAIPOCK	10	EBNA1			523 3.11		0.0028	0.054	

Table 23(b)

006T60-0T559960

09665510-091900

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
S.0005	CTELKLSDY	9	FLU	A	NP	44	1	1.6			
S.0006	STLELRKY	9	FLU	A	NP	377	1	0.020			
S.0044	ILRGSAVHK	9	FLU	A	NP	265	3		1.5	0.0037	
S.0051	RMGNILKCK	9	FLU	A	NP	221	3		0.27	0.062	
S.0046	LMQOSTLPR	9	FLU	A	NP	146	3		0.031	0.10	
S.0048	MIDGIGIFY	9	FLU	A	NP	32	3		0.059	0.0010	
S.0049	MYLSAFDER	9	FLU	A	NP	66	3		0.0016	0.041	
S.0054	YIQMCTELK	9	FLU	A	NP	40	3		0.0031	0.030	
S.0042	QINDRNFWK	9	FLU	A	NP	200	3		0.0028	0.024	
S.0104	SLMQOSTLPR	10	FLU	A	NP	145	3		0.12	0.84	
S.0095	KMIDGIGIFY	10	FLU	A	NP	31	3		0.50	0.0079	
S.0096	ILRGSAVHK	10	FLU	A	NP	264	3		0.36	0.037	
S.0102	RSGAAGAAVK	10	FLU	A	NP	175	3		0.019	0.0046	
S.0108	SSTLELRKY	10	FLU	A	NP	376	3		0.0018	0.016	
S.0103	RSRYWAIKTE	10	FLU	A	NP	382	3		0.012	0	
S.0101	RMVLSAFDER	10	FLU	A	NP	65	3		0.0014	0.010	
S.0061	FYIQMCTEL	9	FLU	A	NP	39	24				2.9
S.0060	AYERMGNIL	9	FLU	A	NP	218	24				0.031
S.0112	RFYIQMCTEL	10	FLU	A	NP	38	24				0.15

Table 23(c)

0965540-091900

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Acid	A1	A3.2	A11	A24
1.0155	LLDTASALY	9	HBV	adr	CORE	420	1	25	0.0007	0	
1.0186	SLDVSAAFY	9	HBV	adr	POL	1001	1	17.2	0.0037	0.0008	
2.0125	PTTGRTSLY	9	HBV	ALL		1,382	1	1.3	0.0008	0	
2.0126	MSPTDLEAY	9	HBV	adr		1,521	1	0.85	<0.0008	0	
1.0208	PTTGRTSLY	9	HBV	adr	POL	1382	1	0.77	0	0	
1.0387	LTQQLNLNLY	9	HBV	adw	POL	1280	1	0.50	0.0008	0.0075	
2.0122	LTQQLNLNLY	9	HBV	adw		1,280	1	0.093			
1.0166	KVGNFTCLY	9	HBV	adr	POL	629	1	0.068			
2.0127	MSPTDLEAY	9	HBV	adw		1,550	1	0.067			
2.0120	PSQFSRGNY	9	HBV	ayw		984	1	0.057			
2.0112	PSWAFKAY	9	HBV	adw		316	1	0.054			
2.0119	QSAVRKEAY	9	HBV	adw		881	1	0.025			
1.0174	PLDKGDKPY	9	HBV	adr	POL	698	1	0.019			
1.0378	SLMILYKTY	9	HBV	adw	POL	1092	1	0.017			
2.0115	ASRDLYVSY	9	HBV	ayw		499	1	0.013			
2.0124	PSRCRLGLY	9	HBV	adr/adw		1,364	1	0.011			
2.0121	SSTSRNINY	9	HBV	adr		1,036	1	0.0097			
1.0519	DLIDTASALY	10	HBV	adr	CORE	419	1	11.1	0	0	
1.0513	LLDPFVRGLY	10	HBV	adr	ENV	120	1	6.3	0.17	0	
2.0239	SLDVSAAFY	10	HBV	ALL		1,000	1	4.2	<0.0008	0.0037	
1.0911	FLCQQLHLY	10	HBV	adr	POL	1250	1	1.1	0.014	0.0048	0.0017
2.0216	QTFGRKLHLY	10	HBV	ayw	POL	1087	1	1.1	0.0056	0.012	
2.0244	KTYGRKLHLY	10	HBV	adw		1,088	1	0.69	0.59	0.22	0
1.0991	KTYGRKLHLY	10	HBV	adw	POL	1088	1	0.57	0.53	0.35	0.0001
2.0242	QTFGRKLHLY	10	HBV	ayw		1,087	1	0.37	0.0037	0.011	
1.0556	KTFGRKLHLY	10	HBV	adr	POL	1069	1	0.34	0.094	0.080	0
2.0341	KTFGRKLHLY	10	HBV	adr		1,069	1	0.30	0.15	0.085	0
1.0766	LQOPRVKALY	10	HBV	adw	ENV	120	1	0.21	0.014	0	
1.0806	TTPAQGTSNY	10	HBV	adw	ENV	288	1	0.20	0	0	
2.0240	LSSTSRNINY	10	HBV	adr		1,035	1	0.20	<0.0008	0	
1.0541	PLDKGDKPY	10	HBV	adr	POL	698	1	0.16	0	0	
2.0238	HSASFGCSFY	10	HBV	ayw		767	1	0.15	0.019	0.017	0
1.0795	FLTQQLNLNLY	10	HBV	adw	POL	1279	1	0.12	0	0	
2.0237	RSASFGCSFY	10	HBV	adr/adw		738	1	0.11	0.033	0.020	0
1.0774	WLWQMDIDPY	10	HBV	adw	CORE	416	1	0.081			
2.0233	TTPAQGTSNY	10	HBV	ayw		288	1	0.066			
1.0542	HTLWKAGILY	10	HBV	adr	POL	723	1	0.030			
2.0231	TSQFPFCGY	10	HBV	adr		226	1	0.018			
2.0246	KSVQHLESY	10	HBV	adw		1,161	1	0.016			
1.0910	NLYYSULLLY	10	HBV	adr	POL	1059	1	0.015			
1.0901	WMWVWYWCPSL	10	HBV	adr	ENV	359	2.1	0.0009	0.019	0	0.0008
2.0089	LLYQTGRK	9	HBV	ayw	POL	1084	3		1.8	0.44	
2.0116	IMPARFYPK	9	HBV	ayw		713	3		0.99	1.5	
2.0082	CLHQSPVKK	9	HBV	ayw	POL	867	3		0.14	0.025	
5.0056	SAKSVVRR	9	HBV		POL	531	3		<0.0003	0.067	
2.0077	HLHQIHK	9	HBV	ayw	POL	686	3		0.041	0.0375	
2.0219	SLPQEHQK	10	HBV	ayw	POL	1197	3		0.36	4.2	
2.0234	SMFPSCCCTK	10	HBV	adr/adw		295	3		0.43	1.9	
2.0235	SMYPSCCCTK	10	HBV	ayw		295	3		1.1	1.79	
5.0107	QAFTPSPTYK	10	HBV		POL	645	3		0.15	1.3	
2.0214	LLLYQTGRK	10	HBV	ayw	POL	1083	3		0.89	0.021	
2.0245	YMDQVVLGAK	10	HBV	ALL		1,123	3		0.16	0.0276	
5.0108	TSKSVVRR	10	HBV		POL	530	3		0.0006	0.013	
2.0094	PTYKAFLOK	9	HBV	ayw	POL	1263	11		0.030	0.085	
2.0068	PTDLEAYFK	9	HBV	adw	"X"	1582	11		0.0002	0.016	
2.0061	KYTSFPWLL	9	HBV	ALL		1,330	24				3.6
2.0059	LYAAVTNPL	9	HBV	adw		1,169	24				3.2
2.0046	FYPNLTLYL	9	HBV	adr		689	24				2.1
2.0045	LYSSTVPF	9	HBV	adw/ayw		665	24				1.9
2.0048	FYPKVTLYL	9	HBV	ayw		718	24				1.7
2.0049	FYPNVTLYL	9	HBV	adw		718	24				1.6
2.0039	LYSILSPFL	9	HBV	ayw		368	24				0.50
2.0044	LYSSTVPVL	9	HBV	adr		636	24				0.37
2.0038	LYNLSPL	9	HBV	adr		368	24				0.34
2.0051	NYRVSWPKF	9	HBV	ayw		991	24				0.18
2.0050	HYQTRHYL	9	HBV	adw/ayw		743	24				0.15
2.0047	HYFKTRHYL	9	HBV	adr		714	24				0.057
2.0060	CYPALMPY	9	HBV	ALL		1,224	24				0.049
5.0062	AYRPPNAPI	9	HBV		NUC/NUCFL	131	24				0.026
2.0054	LYQTGRKL	9	HBV	ayw		1,085	24				0.014
2.0043	SYQHFRL	9	HBV	ayw		607	24				0.011
2.0181	LYSHPIILGF	10	HBV	ALL		1,077	24				1.1
2.0182	LYAAVTNPL	10	HBV	adw		1,169	24				0.32
2.0188	LYRPLSLPF	10	HBV	adr		1,371	24				0.25

Table 23(d)

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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Lotif	A1	A3.2	A11	A24
2.0174	SYQHPRKLL	10	HBV	ayw		407	24				0.16
2.0173	SYQHPRKLL	10	HBV	adr/edw		578	24				0.064
2.0176	YYPEHLVNHV	10	HBV	ayw		735	24				0.040
2.0172	AYRI PNAPIL	10	HBV	ALL		521	24				0.022
2.0171	CYRWMLRRF	10	HBV	ALL		234	24				0.011
5.0115	NFLSLGHL	10	HBV		POL	572	24				0.0099
1.0377	YVSLMLLYK	9	HBV	adw	POL	1090	3.11		0.31	7.4	
1.0189	LLYKTPGRK	9	HBV	adr	POL	1066	3.11		5.0	0.30	
1.0379	LLYKTYGRK	9	HBV	adw	POL	1095	3.11		2.5	0.40	
1.0370	VTKYLPDLK	9	HBV	adw	POL	722	3.11		0.014	1.3	
1.0176	RHYLHTLWK	9	HBV	adr	POL	719	3.11		1.2	0.010	
1.0367	STVPSNPK	9	HBV	adw	POL	668	3.11		0.021	0.93	
1.0215	TTDLAAYPK	9	HBV	adr	"X"	1523	3.11		0.0006	0.92	
1.0848	YVSLMLLYK	9	HBV	adr	POL	1061	3.11		0.39	0.92	
1.0383	PTYKAPLTK	9	HBV	adw	POL	1274	3.11		0.17	0.71	
1.0987	HLYPVARQR	9	HBV	adr	POL	1257	3.11		0.54	0.0020	
1.0356	STNRQLGRK	9	HBV	adw	ENV	85	3.11		0.51	0.34	
1.0991	ALRFTSARR	9	HBV	adr	"X"	1488	3.11		0.44	<0.0005	
1.0197	PVNRFDWK	9	HBV	adr	POL	1197	3.11		0.080	0.41	
1.0369	TVNENRLK	9	HBV	adw	POL	703	3.11		0.016	0.40	
1.1041	VVNHYPQTE	9	HBV	adw	POL	740	3.11		0.030	0.33	
1.0152	STSTGRK	9	HBV	adr	ENV	277	3.11		0.011	0.29	
1.0213	QVLPGLHK	9	HBV	adr	"X"	1505	3.11		0.10	0.28	
1.0172	LTQYLPDLK	9	HBV	adr	POL	693	3.11		0.0039	0.23	
1.0374	CUHQSAVRK	9	HBV	adw	POL	878	3.11		0.22	0.017	
1.0980	VVDPSQSR	9	HBV	adr	POL	963	3.11		0.011	0.30	
1.0382	FLYACQAK	9	HBV	adw	POL	1259	3.11		0.18	0.034	
2.0074	YVNTNMGLK	9	HBV	ayw	CORE	507	3.11		0.16	0.048	
1.0199	FLYACQK	9	HBV	adr	POL	1230	3.11		0.11	0.018	
1.0972	RLADEGLNR	9	HBV	adr	POL	601	3.11		0.10	0.025	
1.0976	AVNHYPKTR	9	HBV	adr	POL	711	3.11		0.0071	0.098	
1.0975	RLKQMPAR	9	HBV	adr	POL	680	3.11		0.095	0.0002	
1.0977	ILYKRETR	9	HBV	adr	POL	730	3.11		0.095	<0.0005	
1.0993	KVPVLGGGR	9	HBV	adr	"X"	1548	3.11		0.042	0.082	
1.0165	NVSPWTHK	9	HBV	adr	POL	621	3.11		0.072	0.076	
1.0982	LLYKTPGR	9	HBV	adr	POL	1065	3.11		0.072	0.0045	
1.0978	RLVPQTSTR	9	HBV	adr	POL	757	3.11		0.068	0.0032	
1.0219	FVLGGGRK	9	HBV	adr	"X"	1550	3.11		0.065	0.019	
1.1042	RLVLQTSR	9	HBV	adw	POL	786	3.11		0.064	0.0002	
1.1043	MLLYKTYGR	9	HBV	adw	POL	1094	3.11		0.061	0.0002	
1.0170	TVNEXRLK	9	HBV	adr	POL	674	3.11		0.048	0.037	
1.1045	NLYPVARQR	9	HBV	adw	POL	1286	3.11		0.042	0.0011	
1.1046	LPYRPTCR	9	HBV	adw	POL	1407	3.11		0.021	0	
1.0845	LVSPGVWR	9	HBV	adr	CORE	509	3.11		0.0033	0.020	
1.0981	LVGSGLPK	9	HBV	adr	POL	1022	3.11		0.0008	0.015	
1.0967	HISCLTGR	9	HBV	adr	CORE	494	3.11		0.013	0.011	
1.1047	SVPSRLPK	9	HBV	adw	POL	1424	3.11		0.0007	0.010	
1.0989	SVPSHLPK	9	HBV	adr	POL	1395	3.11		0.0004	0.010	
1.0564	TLPGHIVLK	10	HBV	adr	POL	1179	3.11		0.092	5.6	
2.0205	TVPVFNPHWK	10	HBV	ayw	POL	669	3.11		0.0067	4.2	
1.0543	TLWKACILYK	10	HBV	adr	POL	724	3.11		3.5	1.0	
1.0807	SMYPSGCTK	10	HBV	ayw	ENV	295	3.11		1.5	3.4	
1.1153	RLPYRPTCR	10	HBV	adw	POL	1406	3.11		2.8	0.030	
1.0584	STDLAAYPK	10	HBV	adr	"X"	1522	3.11		0.0066	2.7	
1.0554	LLLYKTPGRK	10	HBV	adr	POL	1065	3.11		2.5	0.012	
1.0799	TVNAHRLPK	10	HBV	adw	"X"	1529	3.11		0.82	0.46	
1.0546	EAYPKDCLFK	10	HBV	adr	"X"	1527	3.11		0.037	0.74	
1.1081	LVDPSQSR	10	HBV	adr	POL	962	3.11		0.0009	0.63	
1.0789	MLLYKTYGRK	10	HBV	adw	POL	1094	3.11		0.61	0.020	
1.0546	TAYSHLTSK	10	HBV	adr	POL	858	3.11		0.26	0.092	
1.0562	SLGHLNPNK	10	HBV	adr	POL	1150	3.11		0.20	0.078	
1.1152	RLGLYRPLR	10	HBV	adw	POL	1397	3.11		0.19	0.0049	
1.0547	VTGGVFLVDK	10	HBV	adr	POL	943	3.11		0.035	0.17	
1.1150	RIRTPPAR	10	HBV	adw	POL	962	3.11		0.17	0.0002	
1.0561	TVNGHQVLPK	10	HBV	adr	"X"	1500	3.11		0.073	0.092	
1.1091	SLPPQPTCR	10	HBV	adr	POL	1377	3.11		0.077	0.043	
1.1072	TLPETTVVRR	10	HBV	adr	CORE	532	3.11		<0.0003	0.075	
1.1089	CTDNSVLSR	10	HBV	adr	POL	1320	3.11		0.025	0.072	
1.1071	STLPETTVVR	10	HBV	adr	CORE	531	3.11		0.0005	0.068	
2.0210	KVTKYLPDLK	10	HBV	ayw	POL	721	3.11		0.027	0.053	
1.1148	STRHGDKSFR	10	HBV	adw	POL	792	3.11		0.0057	0.038	
1.0935	VLSCWWLQFR	10	HBV	adw	POL	923	3.11		0.029	0.0087	
1.0781	NVTKYLPDLK	10	HBV	adw	POL	721	3.11		<0.0004	0.023	

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.1092	RVCCQLD ⁺ AR	10	HBV	adr	X	1422	3.11		0.0019	0.023	
1.0793	SLGIHLNPOK	10	HBV	adw	POL	1179	3.11		0.017	0.014	
1.0909	YLVSPGVWIR	10	HBV	adr	CORE	508	3.11		0.015	0.0027	
2.0207	FVGPLTVNEK	10	HBV	ayw	POL	698	3.11		0.0057	0.013	
1.0535	YVGPLTVNEK	10	HBV	adr	POL	669	3.11		0.0069	0.014	
1.1075	RLADEGLNRR	10	HBV	adr	POL	401	3.11		0.013	0.0004	
1.1084	IVKLKQCFR	10	HBV	adr	POL	1185	3.11		0.013	0.0024	
1.0773	PIPSWAF ⁺ AK	10	HBV	adw	ENV	314	3.11		<0.0003	0.010	
1.0778	LTVNENRR ⁺ LK	10	HBV	adw	POL	702	3.11		0.0025	0.0095	

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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0118	CTCGSDLY	9	HCV		LORF	1123	1	3.0	0	0.010	
1.0112	NIYDVQYLY	9	HCV		NS1/ENV2	697	1	0.60	0	0.010	
2.0034	VQCCNCSY	9	HCV			302	1	0.54	0.0005	0.0003	
2.0035	LITRDMVDY	9	HCV			605	1	0.078			
1.0145	RVCEGMALY	9	HCV		LORF	2588	1	0.053			
1.0140	DVVCOSMSY	9	HCV		LORF	2416	1	0.039			
2.0036	PTIFQIRMY	9	HCV			636	1	0.012			
1.0509	GLSAPSLHSY	10	HCV		LORF	2888	1	0.41	0.013	0.0034	0.0002
1.0489	TLHGPTPLY	10	HCV		LORF	1617	1	0.30	0.11	0.0024	
2.0037	EYVLLFL	9	HCV			719	24				1.4
2.0169	MYVGGVEHRL	10	HCV			633	24				0.026
2.0170	EYVLLFL	10	HCV			719	24				0.010
1.0139	SVPABLURK	9	HCV		LORF	2269	3,11		0.016	0.07	
1.0955	QLFTSPRR	9	HCV		ENV1	290	3,11		0.75	0.033	
1.0090	RLGVRAIRK	9	HCV		CORE	43	3,11		0.74	0.16	
1.0123	LIPCHSKKK	9	HCV		LORF	1391	3,11		0.54	0.19	
1.0122	HLIPCHSKK	9	HCV		LORF	1390	3,11		0.25	0.010	
1.0952	KTSEISQPR	9	HCV		CORE	51	3,11		0.16	0.064	
1.0120	AVCTEGVAK	9	HCV		LORF	1183	3,11		0.016	0.038	
1.0143	EYCVQPEK	9	HCV		LORF	2563	3,11		0.0019	0.083	
1.0137	ITRVEENK	9	HCV		LORF	2241	3,11		0.015	0.0399	
1.0957	CITSITCR	9	HCV		LORF	1042	3,11		0.0085	0.011	
1.0486	GVAGALVAFK	10	HCV		LORF	1858	3,11		0.07	1.1	
1.0480	HLHAPTCGCK	10	HCV		LORF	1227	3,11		0.57	0.0051	
1.1062	RMVYVGGVEHRL	10	HCV		NS1/ENV2	632	3,11		0.27	0.012	
1.0485	HLIPCHSKKK	10	HCV		LORF	1390	3,11		0.27	0.025	
1.0484	TLGPGAYMSK	10	HCV		LORF	1261	3,11		0.17	0.13	
1.1067	GVGYLLPNR	10	HCV		LORF	3002	3,11		0.0029	0.032	
1.1063	LLFLLADAR	10	HCV		NS1/ENV2	723	3,11		0.015	0	

Table 23(e)

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A3.2	A11	A24
1.0014	FRDYVDRFY	9	HIV		CAG	298	1	0.090			
2.0129	TYQYMDOLY	9	HIV			875	1	0.064			
1.0028	TVLDVGDAY	9	HIV		POL	802	1	0.018			
1.0412	VTVLVDGDAY	10	HIV		POL	801	1	0.28	0	0.0004	
1.0415	VTYQYMDOLY	10	HIV		POL	874	1	0.25	0.0007	0.0090	
2.0252	VTVLVDGDAY	10	HIV			801	1	0.088			
1.0431	EVNTVTDSCY	10	HIV		POL	1187	1	0.053			
1.0441	LVAVHVASGY	10	HIV		POL	1329	1	0.039			
1.0442	PAETQETAY	10	HIV		POL	1343	1	0.013			
2.0251	ISKQENPY	10	HIV			742	1	0.013			
2.0255	QMAVFIHNFK	10	HIV			1,432	3		0.61	0.64	
2.0064	RYLKDDQQL	9	HIV			2,778	24				0.76
2.0134	RYLKDDQQL	9	HIV			2,778	24				0.32
2.0065	TYQYQEPF	9	HIV			1,033	24				0.30
2.0131	TYQYQEPF	9	HIV			1,033	24				0.20
2.0063	TYQEPFKNL	9	HIV			1,036	24				0.052
2.0132	TYQEPFKNL	9	HIV			1,036	24				0.033
2.0066	TYQYMDOLY	9	HIV			875	24				0.013
2.0247	TYKRWILCL	10	HIV			266	24				0.017
2.0190	TYKRWILCL	10	HIV			266	24				0.014
2.0049	LYPLASLSL	10	HIV			506	24				0.014
1.0069	KLAGEWPFYK	9	HIV		POL	1358	3,11		2.7	0.069	
1.0944	AVRIHNFRIK	9	HIV		POL	1434	3,11		0.17	1.8	
1.0082	ALPQSMTK	9	HIV		POL	833	3,11		1.1	0.96	
1.0046	IVWQKTPK	9	HIV		POL	1073	3,11		0.085	0.37	
1.0079	KLTEDRWNK	9	HIV		VIF	1712	3,11		0.013	0.27	
1.0027	GIFHPAGLK	9	HIV		POL	788	3,11		0.23	0.065	
1.0059	QIEQLKK	9	HIV		POL	1215	3,11		0.0091	0.16	
1.0109	KIWPYSYKGR	9	HIV		CAG	443	3,11		0.12	0.0005	
1.0072	QATDQTK	9	HIV		POL	1458	3,11		0.025	0.098	
1.0036	MCYELHPDK	9	HIV		POL	925	3,11		0.064	0.094	
1.0062	YLAWVPAHK	9	HIV		POL	1227	3,11		0.077	0.057	
1.0038	KIWPYSYKGR	9	HIV		CAG	443	3,11		0.077	<0.0005	
1.0067	FVNTPLVK	9	HIV		POL	1111	3,11		0.012	0.066	
1.0024	NTVPFAIKK	9	HIV		POL	732	3,11		0.033	0.060	
1.0080	TVQTHCIK	9	HIV		ENV	2420	3,11		0.0021	0.046	
1.0013	ILDRLQCPK	9	HIV		CAG	287	3,11		0.042	0.0048	
1.0015	RDYVDRFYK	9	HIV		CAG	299	3,11		0.0007	0.040	
1.0058	GKQACPK	9	HIV		POL	1199	3,11		<0.0009	0.040	
1.0064	VFLDCIDK	9	HIV		POL	1254	3,11		0.038	0.032	
1.0026	LVDFRELNK	9	HIV		POL	768	3,11		0.011	0.030	
1.0078	KVYPRKAK	9	HIV		POL	1513	3,11		0.029	0.0039	
1.0942	MTKLEPRK	9	HIV		POL	859	3,11		<0.0008	0.016	
1.0463	TVYTGVPWVK	10	HIV		ENV	2185	3,11		3.8	7.8	
1.0418	TVQPTVLPEK	10	HIV		POL	935	3,11		0.16	5.6	
1.0447	AVRIHNFRIK	10	HIV		POL	1434	3,11		0.46	0.85	
1.0437	KVFLDCIDK	10	HIV		POL	1253	3,11		0.36	0.78	
1.0408	KLVDRELNK	10	HIV		POL	768	3,11		0.51	0.090	
1.0403	KLKPCMDCPK	10	HIV		POL	706	3,11		0.39	0.076	
1.0395	FLGKWPSYK	10	HIV		CAG	440	3,11		0.32	0.024	
1.1054	KQNFRVYYR	10	HIV		POL	1474	3,11		0.032	0.21	
1.0410	GIFHPAGLK	10	HIV		POL	788	3,11		0.011	0.17	
1.0426	LVKLWYQLEK	10	HIV		POL	1117	3,11		0.056	0.082	
1.0398	MKGCGCFIK	10	HIV		POL	642	3,11		0.0099	0.053	
1.0413	MTKLEPRK	10	HIV		POL	859	3,11		0.015	0.038	
1.0453	VVIQONSQIK	10	HIV		POL	1504	3,11		<0.0005	0.021	
1.0394	FLGKWPSHK	10	HIV		CAG	440	3,11		0.020	0.0013	
1.1059	IVQQNNLLR	10	HIV		ENV	2741	3,11		0.0024	0.019	
1.0417	FTTPDKKHQK	10	HIV		POL	909	3,11		<0.0002	0.015	
1.0405	LVECTEMEK	10	HIV		POL	729	3,11		0.0002	0.012	
1.0392	LVQANPDCK	10	HIV		CAG	327	3,11		<0.0002	0.011	

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Table 23(f)

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos	Motif	A1	A3.2	A11	A24
1.0225	ISEYRHYCY	9	HPV	16	E6	80	1	7.8	0.0011	0.036	
1.0230	QAEPRAHY	9	HPV	16	E7	44	1	0.021			
1.0610	LQDEITCVY	10	HPV	18	E6	25	1	0.25	0.0056	0.012	
2.0159	YSKISEYRHY	10	HPV	16	E6	77	1	0.17	<0.0009	0	
2.0162	YSKISEYRHY	10	HPV	16	E6	77	1	0.11	<0.0009	0	
1.0599	HGDTPTLHEY	10	HPV	16	E7	2	1	0.087			
1.0601	QPETDOLYCY	10	HPV	16	E7	16	1	0.033			
1.0913	IHDILECVY	10	HPV	16	E6	30	1	0.032			
2.0160	YSRIELRHY	10	HPV	18	E6	72	1	0.018			
2.0164	YSRIELRHY	10	HPV	18	E6	72	1	0.012			
1.0594	AVCDKCLKFY	10	HPV	16	E6	68	1	0.0095			
2.0161	LLIRCLRCOK	10	HPV	18	E6	101	3		0.081	0.078	
2.0032	HTMLCMCOCK	9	HPV	18	E7	59	11		0.020	0.079	
2.0029	VYCKTVLEL	9	HPV	18	E6	33	24				0.33
2.0027	CYSLYGTL	9	HPV	16	E6	87	24				0.057
2.0024	VYDFAFRDL	9	HPV	16	E6	49	24				0.032
2.0031	LYNLIRCL	9	HPV	18	E6	98	24				0.019
2.0030	VYGDLEKL	9	HPV	18	E6	85	24				0.010
1.0239	SVYGDLEK	9	HPV	18	E6	84	3.11		0.39	2.3	
1.0243	SVYGDLEK	9	HPV	18	E6	84	3.11		0.55	1.1	
1.0244	SVYGDLEK	9	HPV	18	E6	84	3.11		0.70	0.95	
1.0226	TTLEBOQYNK	9	HPV	16	E6	93	3.11		0.010	0.67	
1.0241	SIPHAACHK	9	HPV	18	E6	59	3.11		0.0094	0.25	
1.0237	SIPHAACHK	9	HPV	18	E6	59	3.11		0.017	0.12	
1.0233	IVCPICQK	9	HPV	16	E7	89	3.11		0.035	0.023	
1.0997	KLRHLNEKR	9	HPV	18	E6	117	3.11		0.025	<0.0005	
1.0234	LLIRCLRCOK	9	HPV	18	E6	102	3.11		0.019	0.0012	
1.0853	IILECVYCK	9	HPV	16	E6	33	3.11		0.0016	0.019	
1.0999	CIDFYRIK	9	HPV	18	E6	68	3.11		0.017	0.0018	
1.0998	CIDFYRIK	9	HPV	18	E6	68	3.11		0.010	0.0009	
1.0596	GTTLEBOQYNK	10	HPV	16	E6	92	3.11		0.010	0.98	
1.0606	LLIRCLRCOK	10	HPV	18	E6	101	3.11		0.076	0.29	
1.0598	LLIRCLRCOK	10	HPV	16	E6	106	3.11		0.12	0.24	
1.0629	LLIRCLRCOK	10	HPV	18	E6	101	3.11		0.16	0.11	
1.0614	LTEVFEFAK	10	HPV	18	E6	41	3.11		0.0009	0.11	
1.0605	GVCPICQK	10	HPV	16	E7	88	3.11		0.0017	0.060	
1.0625	LTEVFEFAK	10	HPV	18	E6	41	3.11		0.0012	0.061	
1.0591	DILECVYCK	10	HPV	16	E6	32	3.11		0.0065	0.021	
1.1101	KLRHLNEKR	10	HPV	18	E6	117	3.11		0.013	0	
1.1095	CVYCKQQLR	10	HPV	16	E6	37	3.11		0.011	0.0059	

Table 23(g)

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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A32	A11	A24
2.0020	EVDPIGHLY	9	MAGE	3		161	1	18	0.0002	0.0009	
3.0172	EADPTSNLY	9	MAGE	5/51		161	1	9.9	0.0006	0.0006	0
1.0258	TQDLVQEKY	9	MAGE	1		240	1	2.1	0	0.0002	
3.0173	EVDPIGHVY	9	MAGE	6		161	1	1.9	<0.0002	<0.0002	0
1.0254	EADPTCHSY	9	MAGE	1		161	1	1.1	0	0	
1.0259	LVQEKYLEY	9	MAGE	1		243	1	0.42	0.0013	0.053	
6.0053	TSYVKYLEY	9	MAGE	1	new	275	1	0.099			
2.0009	SSLPTTMNY	9	MAGE	3		9	1	0.053			
2.0011	GSVVGNIWQY	9	MAGE	3		77	1	0.050			
2.0008	SSPTTINY	9	MAGE	2		9	1	0.043			
1.0252	MLESVIKNY	9	MAGE	1		128	1	0.011			
2.0147	ASSLPTTMNY	10	MAGE	3		8	1	2.6	<0.0009	0.033	
2.0167	LTQDLVQEKY	10	MAGE	1		239	1	1.2	<0.0009	0.0073	
6.0114	ETSYVKYLEY	10	MAGE	1	new	274	1	0.56			
2.0141	ASSPTTINY	10	MAGE	2		8	1	0.17	<0.0009	0.026	
1.0648	DLVQEKYLEY	10	MAGE	1		242	1	0.044			
6.0065	TSYVKYLEY	9	MAGE	1	new	275	3		0.71	0.010	
4.0119	TTINPTRQR	9	MAGE	1		66	3		0.043	0.37	
6.0064	ALAETSYVK	9	MAGE	1	new	271	3		0.31	0.36	
4.0132	LTQDLVQEK	9	MAGE	1		239	3		<0.0008	0.14	
6.0063	LVQEKYLEY	9	MAGE	1	new	243	3		0.0026	0.034	
4.0131	HSAYGEPRK	9	MAGE	1		229	3		0.014	0.0009	
4.0122	LFRAVITTK	9	MAGE	1		97	3		0.011	0.0005	
6.0124	RVRFFPSLR	10	MAGE	1	new	290	3		0.43	0.0089	
4.0161	ADLVCFLLK	10	MAGE	1		107	3		0.35	0.29	
4.0160	ESLRAVITK	10	MAGE	1		95	3		0.14	0.088	
6.0119	DLVQEKYLEY	10	MAGE	1	new	242	3		0.032	0.0051	
6.0123	YVIKVSARVR	10	MAGE	1	new	283	3		0.019	0.0009	
4.0168	LSVMEVYDGR	10	MAGE	1		218	3		<0.0008	0.012	
4.0163	KAEMLESVIK	10	MAGE	1		125	3		<0.0003	0.0097	
6.0125	RALAETSYVK	10	MAGE	1	new	270	11		0.18	0.24	
2.0010	NYPLWSQSY	9	MAGE	3		16	24				0.027
2.0165	NYIHKPFPIF	10	MAGE	1		135	24				0.25
2.0151	LYPATCLCL	10	MAGE	3		115	24				0.048
6.0126	SYVKVLEYVI	10	MAGE	1	new	276	24				0.036
1.0248	SLRAVITK	9	MAGE	1		96	3,11		4.1	2.7	
1.1006	SVMEVYDGR	9	MAGE	1		219	3,11		0.0083	1.3	
1.1004	TTINPTRQR	9	MAGE	1		66	3,11		0.016	1.0	
1.0257	LTQDLVQEK	9	MAGE	1		239	3,11		0.0002	0.38	
1.0634	SLRAVITKK	10	MAGE	1		96	3,11		1.2	0.98	
1.0647	LTQDLVQEK	10	MAGE	1		238	3,11		0.0004	0.16	
1.0640	MLESVIKNYK	10	MAGE	1		128	3,11		0.14	0.027	
1.0644	LLGDNQMPK	10	MAGE	1/3		182	3,11		0.020	0.011	
1.0630	SLBQRSUHK	10	MAGE	1		2	3,11		0.015	0.015	

Table 23(h)

Peptide	Sequence	AA	Virus	Strain	Molecule	P.	Mottf	A1	A3.2	A11	A26
1.0281	CSDCITTHY	9	p53			226	1	29.5	0.0010	0.029	
1.0667	CTAKSVTCTY	10	p53			117	1	0.33	0.023	0.049	0
1.0672	RVEGNLRVEY	10	p53			196	1	0.022			
1.0278	RVRAMAIYK	9	p53			156	3.11		1.5	0.73	
1.0276	CTYSPALNK	9	p53			124	3.11		0.46	1.1	
1.0285	NTSSSPQPK	9	p53			311	3.11		0.0009	0.095	
1.0284	RTEENLRK	9	p53			283	3.11		0.0015	0.091	
1.0287	ELNEALELK	9	p53			343	3.11		0.020	0.0052	
1.0678	RTEENLRKK	10	p53			283	3.11		3.3	0.0080	
1.1113	KTYQCSYCFR	10	p53			101	3.11		2.6	0.88	
1.1115	VVRKCPHER	10	p53			172	3.11		0.099	0.0017	
1.0679	NTSSSPQPKK	10	p53			311	3.11		0.0035	0.054	
1.1121	RVCACFGRDR	10	p53			273	3.11		0.014	0.011	
1.1116	GLAPFOHLIR	10	p53			187	3.11		0.013	0.0006	

Table 23(i)

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006160-01559360

Peptide	Sequence	AA	Virus	Strain	Molecule	Pos.	Motif	A1	A32	A11	A24
3.0173	KGEYFVEMY	9	PAP			322	1	14	<0.0002	0.0002	0
3.0174	LCSEYTRKY	9	PAP			81	1	0.78	<0.0002	0.0002	0
3.0166	ASCHLTLY	9	PAP			311	1	0.77	<0.0002	0.055	0
3.0163	ESYKHEQVY	9	PAP			95	1	0.098	<0.0002	0.0002	0
3.0237	LSLSLSLY	10	PAP			238	1	14	0.0028	0.0004	0
3.0235	LSLSLSLY	10	PAP			238	1	12	0.0005	0.0004	0
3.0236	LTQLCMQHY	10	PAP			70	1	0.62	0.015	0.0024	0.0022
3.0238	KGEYFVEMY	10	PAP			322	1	0.018			
3.0230	LVNEILNHMK	10	PAP			263	3		0.056	0.12	
3.0158	ATQPSYK	9	PAP			274	11		0.10	1.2	
3.0231	ETLKSEERQK	10	PAP			170	11		<0.0004	0.014	
3.0161	LYPEKGEYF	9	PAP			318	24				2.5
3.0160	LYCESYHNF	9	PAP			213	24				0.44
3.0159	PYKDFIATL	9	PAP			183	24				0.11
3.0162	VYNGLLPPY	9	PAP			302	24				0.032
3.0232	PYASCHLTLY	10	PAP			309	24				0.024

Table 23(j)

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Peptide	Sequence	AA	Virus	Strain	Molecule	Pos. Motif	A1	A3.2	A11	A24
1.0270	ALPERISLY	9	PSA			231 1	0.011			
2.0157	VSHSPHPLY	10	PSA			88 1	0.15	<0.0003	0.0015	
1.0285	PLYDMSLLK	9	PSA			95 3.11		0.24	0.007	
1.0273	VVHYRKWIK	9	PSA			242 3.11		0.0072	0.093	
1.0272	YTKVVHYRK	9	PSA			239 3.11		0.0006	0.058	
1.1009	SLIGNRFLR	9	PSA			100 3.11		0.0024	0.047	
1.0280	IVCGWCEK	9	PSA			21 3.11		0.041	0.019	
1.0269	QVHPQKVTK	9	PSA			182 3.11		0.0060	0.014	
1.1112	SLYTKVVHYR	10	PSA			237 3.11		0.28	0.23	
1.0653	LTAAHQIRNK	10	PSA			57 3.11		0.14	0.083	
1.0651	RIVCGWCEK	10	PSA			20 3.11		0.046	0.067	
1.0642	KVVHYRKWIK	10	PSA			241 3.11		0.045	0.045	
1.1111	VTKRMLCAGR	10	PSA			188 3.11		0.0003	0.012	
3.0108	MLRLSEPA	9	PSA			118 Random				

Table 23(k)

006T60" 07559960

TABLE 24: CTL EPTOPES IDENTIFIED IN PEPTIDE SCREENING.

S qu nc	Antigen	Motif	Id
EVDPIGHLY	MAGE3	A01	1044.07
ASSLEPTMNY	MAGE3	A01	1044.01
EADPTGHSY	MAGE1	A01	958.01
SSLEPTMNY *	MAGE3	A01	1072.02*
GSVGNWQY *	MAGE3	A01	1072.03*
ALAETSYVK *	MAGEIN	A03	1072.38*
SLERAVITK	MAGE1	A11	1072.13
RALAETSYVK	MAGEIN	A11	1072.39
ESLERAVITK	MAGE1	A11	1072.15
KVYLAWPRAHK	HIV	A3/11*	1069.42*
TVYYGVPEVMK	HIV	A03	1069.43
KLGRWPEVK	HIV	A03	1069.44
KMIGGIGFEIK	HIV	A03	1069.45
ALFQSSMTK	HIV	A03	966.01
WTYQIYQEPFK	HIV	A03	1069.46
FLGRIWPSHK *	HIV	A03	1069.56*
TVYYGVPEVMK	HIV	A11	1052.03
VTVYYGVPEVMK	HIV	A11	1069.47
GVAGALVAEK	HCV	A03	1073.10
CTCGSSDLY	HCV	A11	1069.62
GVAGALVAEK	HCV	A11	1052.05
LIDTASALY *	HBV	A01	1069.01*
TLWKAGILYK	HBV	A03	1069.15
• borderline positive			

09665510.091900

Table 25 a
Peptides Synthesized
by Cytel For Loading
Onto Acid Stripped
Autologous PBMCs and
PHA Blasts

	Peptide ID #	Antigen	Sequence
	777.03	HBs	FLLTRILTI
10	924.07	HBC	FLPSDFFPSV
	927.32	HBp	GLYSSTVPV
	938.01	MAGE 1	EADPTGHSY
	939.03	PSA	VLVHPQWVL
	941.01	HBC	FLPSDYFPSV
15	1044.04	PAP	ILLWDPIPV
	1044.05	PSA	KLQCVDLVHI
	1044.06	PSA	MLLRLSEPAEL

20 Table 25 b
Cell Population

	¹²⁵ I-Labeled	CPMS	
	Peptide +/- Cold	+/- std. dev.	
	Peptide		
	- cold peptide	3553 ± 157	n = 3
25	+ cold peptide	13	n = 1
	-cold peptide	370 ± 37	n = 3
	+ cold peptide	50	n = 1

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